STIC-Biotech/ChemLib

From: Snedden, Sheridan
Sent: Tuesday, August 19, 2003 6:48 PM
To: STIC-Biotech/ChemLib
Subject: Seq Search 09820053

Sheridan SNEDDEN ID# **79298** Date: **8/19 /2003**
AU **1653**
308-4843
Serial # : 09820053
Room Location: **10A12**
Mail Box: **9B01**

Claims reads: Peptide 5 to 23 amino acids length, 70% identical to SEQ ID NO: 43, wherein 80% of the amino acids are Phe, Lys, Leu and Ala.

I am not sure how to request this search. Please advise.

Thanks,
Examiner Snedden
#79298
A.U. 1653/ 9B01
Office Location: 10A12
Phone #: 305-4843

Searcher: D. Sheppard
Phone: 305-4321
Location: CM1 6A03
Date Picked Up:
Date Completed: 8/22
Searcher Prep/Review: 15
Clerical:
Online time: 6

TYPE OF SEARCH:
NA Sequences:
AA Sequences: 1
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.: Geneseq
WWW/Internet:
Other (specify):

STIC Search Report
Biotech-Chem Library

STIC Database Tracking

TO: Sheridan Snedden
Location: CM1/10A12&9B01
Art Unit: 1653
Friday, August 22, 2003

Case Serial Number: 09/820053

From: David Schreiber
Location: Biotech-Chem Library
CM1-6A03
Phone: 308-4292

david.schreiber@uspto.gov

Search Notes

Sheridan,

Since this specifically refers to seq 43 and that sequence has the preferred residues, it seemed the best way to run this was just by doing a standard search of seq 43 and saving 45 alignments so you can see what you got. Hope this helps. Call if you have any questions.

David Schreiber
308-4292

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 21, 2003, 08:17:40 ; Search time 28 Seconds
(without alignments)
22.667 Million cell updates/sec

Title: US-09-820-053A-43
Perfect score: 66
Sequence: 1 FAKALKALLKALKAL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 168489

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	77.3	21	1	US-07-908-455A-6	Sequence 6, Appli
2	51	77.3	21	1	US-08-434-120-32	Sequence 32, Appl
3	51	77.3	21	1	US-08-465-325-32	Sequence 32, Appl
4	51	77.3	21	4	US-09-115-737-32	Sequence 32, Appl
5	50	75.8	14	1	US-08-944-133-16	Sequence 16, Appl
6	50	75.8	14	1	US-08-944-133-33	Sequence 33, Appl
7	50	75.8	21	1	US-08-944-133-17	Sequence 17, Appl
8	50	75.8	21	1	US-08-944-133-30	Sequence 30, Appl
9	50	75.8	21	1	US-08-944-133-34	Sequence 34, Appl
10	48	72.7	23	1	US-08-231-730A-39	Sequence 39, Appl
11	48	72.7	23	1	US-08-427-001C-44	Sequence 44, Appl
12	48	72.7	23	1	US-08-457-171-39	Sequence 39, Appl
13	48	72.7	23	2	US-08-724-306-19	Sequence 19, Appl
14	48	72.7	23	2	US-08-505-486-44	Sequence 44, Appl
15	48	72.7	23	3	US-08-689-489C-39	Sequence 39, Appl
16	48	72.7	23	3	US-08-801-028-44	Sequence 44, Appl
17	48	72.7	23	3	US-09-340-154-44	Sequence 44, Appl
18	48	72.7	23	3	US-09-232-802A-39	Sequence 39, Appl
19	48	72.7	23	4	US-09-482-611B-44	Sequence 44, Appl
20	48	72.7	23	4	US-09-019-922A-44	Sequence 44, Appl
21	48	72.7	23	5	PCT-US94-12550-47	Sequence 47, Appl
22	48	72.7	23	5	PCT-US95-04335-39	Sequence 39, Appl
23	48	72.7	23	5	PCT-US95-04718-39	Sequence 39, Appl
24	48	72.7	23	5	PCT-US95-09338-44	Sequence 44, Appl
25	48	72.7	23	5	PCT-US95-09339-44	Sequence 44, Appl
26	48	72.7	23	5	PCT-US96-10041-19	Sequence 19, Appl
27	40	60.6	21	1	US-07-908-455A-8	Sequence 8, Appli
28	40	60.6	21	1	US-08-434-120-34	Sequence 34, Appl
29	40	60.6	21	1	US-08-465-325-34	Sequence 34, Appl
30	40	60.6	21	4	US-09-115-737-34	Sequence 34, Appl
31	39	59.1	22	3	US-08-752-526-3	Sequence 3, Appli
32	39	59.1	23	1	US-08-231-730A-42	Sequence 42, Appl
33	39	59.1	23	2	US-08-505-486-47	Sequence 47, Appl
34	39	59.1	23	3	US-08-689-489C-42	Sequence 42, Appl
35	39	59.1	23	3	US-08-801-028-47	Sequence 47, Appl
36	39	59.1	23	3	US-09-340-154-47	Sequence 47, Appl
37	39	59.1	23	3	US-09-232-802A-42	Sequence 42, Appl
38	39	59.1	23	4	US-09-482-611B-47	Sequence 47, Appl
39	39	59.1	23	5	PCT-US95-04718-42	Sequence 42, Appl
40	39	59.1	23	5	PCT-US95-09338-47	Sequence 47, Appl
41	39	59.1	23	5	PCT-US95-09339-47	Sequence 47, Appl
42	38	57.6	14	1	US-08-232-455A-31	Sequence 31, Appl
43	38	57.6	14	1	US-08-944-133-29	Sequence 29, Appl
44	38	57.6	21	1	US-07-908-455A-7	Sequence 7, Appli
45	38	57.6	21	1	US-08-434-120-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-07-908-455A-6
; Sequence 6, Application US/07908455A
; Patent No. 5459237
; GENERAL INFORMATION:
; APPLICANT: Berkowitz, Barry A.
; APPLICANT: Kari, U. Prasad
; APPLICANT: Malov, W. Lee
; TITLE OF INVENTION: No. 54,225/01 Peptide Compositions and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi & Stewart
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: FW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,455A
; FILING DATE: 19920702
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07686115
; FILING DATE: 15-APR-1991
; APPLICATION NUMBER: US 07176629
; FILING DATE: 08-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 421250-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201 994 1744
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: amide-terminated
US-07-908-455A-6

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  Query Match             77.3%;  Score 51;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.2;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              :|||||| ||||||
Db          4 SKALKALSKALKAL 17


RESULT 2
US 08/434,120-32
; Sequence 32, Application US/08434120
; Patent No. 5635479
;  GENERAL INFORMATION:
;    APPLICANT:  Baker, Margaret A.
;    APPLICANT:  Jacob, Leonard S.
;    APPLICANT:  Maloy, W. Lee
;    TITLE OF INVENTION:  Treatment of Gynecological
;    TITLE OF INVENTION:  Malignancies with
;    TITLE OF INVENTION:  Biologically Active Peptides
;    NUMBER OF SEQUENCES:  117
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi & Stewart
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  DW4.V2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/434,120
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/297,950
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/226,108
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/937,462
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  121359.194
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 994 1700
;      TELEFAX:  201-994 1744
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US 08/434,120-32

  Query Match             77.3%;  Score 51;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.2;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              :|||||| ||||||
Db          4 SKALKALSKALKAL 17


RESULT 3
US-08/465,425-32
; Sequence 32, Application US/08465425
; Patent No. 5686563
;  GENERAL INFORMATION:
;    APPLICANT:  Magainin Pharmaceuticals Inc.
;    APPLICANT:  5110 Campus Drive
;    APPLICANT:  Plymouth Meeting, PA  19462
;    TITLE OF INVENTION:  Biologically Active Peptides Having
;    TITLE OF INVENTION:  N-Terminal Substitutions
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W. Suite 700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,425
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/184,402
;      FILING DATE:  18-JAN-94
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/891,201
;      FILING DATE:  01-JUN-92
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fordis, Jean F.
;      REGISTRATION NUMBER:  32,984
;      REFERENCE/DOCKET NUMBER:  05307.0021-00CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US 08/465,425-32

  Query Match             77.3%;  Score 51;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.2;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              :|||||| ||||||
Db          4 SKALKALSKALKAL 17


RESULT 4
US 09/115,737-32
; Sequence 32, Application US/09115737
; Patent No. 6348445
;  GENERAL INFORMATION:
;       APPLICANT: D. Prasad Kati
;                  Jaffy J. Williams
;                  Michael McLane
;       TITLE OF INVENTION: Biologically Active Peptides With Reduced
;                           Toxicity in Animals and a Method for Preparing
;       NUMBER OF SEQUENCES: 156
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
;                       Dunner, L.L.P.
;            STREET: 1300 I Street, N.W. Suite 70
;            CITY: Washington
;            STATE: D.C.
```

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;               COUNTRY: USA
;               ZIP: 20005-3315
;          COMPUTER READABLE FORM:
;               MEDIUM TYPE: Floppy disk
;               COMPUTER: IBM PC compatible
;               OPERATING SYSTEM: PC-DOS/MS-DOS
;               SOFTWARE: PatentIn Release #1.0, Version #1.3
;          CURRENT APPLICATION DATA:
;               APPLICATION NUMBER: US/09/115,737
;               FILING DATE: 15-Jul-1998
;               CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;               APPLICATION NUMBER: 08/465,330
;               FILING DATE: 05-JUN-1995
;               APPLICATION NUMBER: 08/184,462
;               FILING DATE: 18-JAN-94
;               APPLICATION NUMBER: 07/891,201
;               FILING DATE: 01-JUN-92
;          ATTORNEY/AGENT INFORMATION:
;               NAME: Fordis, Jean B
;               REGISTRATION NUMBER: 32,984
;               REFERENCE/DOCKET NUMBER: 05387.0021-06000
;          TELECOMMUNICATION INFORMATION:
;               TELEPHONE: (202) 408-4000
;               TELEFAX: (202) 408-4400
;     INFORMATION FOR SEQ ID NO: 32:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 21 amino acids
;               TYPE: amino acid
;               TOPOLOGY: linear
;          MOLECULE TYPE: peptide
;          SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-115-737-32

  Query Match             77.3%;  Score 51;  DB 4;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.2;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           2 AKALKALLKALKAL 15
               :|||||| ||||||
Db           4 SKALKALSKALKAL 17


RESULT 5
US-08-944-133-16
; Sequence 16, Application US/08944133
; Patent No. 5789542
;  GENERAL INFORMATION:
;     APPLICANT:  McLaughlin, Mark L
;     APPLICANT:  Becker, Calvin L
;     TITLE OF INVENTION:  Amphipathic Peptides
;     NUMBER OF SEQUENCES:  54
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  John H. Runnels
;       STREET:  P. O. Box 2471
;       CITY:  Baton Rouge
;       STATE:  LA
;       COUNTRY:  USA
;       ZIP:  70821-2471
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/944,133
;       FILING DATE:  06-OCT-1997
;       CLASSIFICATION:  5530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/789,077
;       FILING DATE:  03-FEB-1997
;       APPLICATION NUMBER:  US/08/681,075
;       FILING DATE:
;       APPLICATION NUMBER:  US/08/232,525
;       FILING DATE:  22-APR-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Runnels, John H
;       REGISTRATION NUMBER:  33451
;       REFERENCE/DOCKET NUMBER:  Atty File No. 5789542 9301
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  504 387-4221
;       TELEFAX:  504 346-8049
;   INFORMATION FOR SEQ ID NO:  16:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  14 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-944-133-16

  Query Match             75.8%;  Score 50;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 0.19;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           3 KALKALLKALKAL 15
               |||||| ||||||
Db           1 KALKALEKALKAL 13


RESULT 6
US-08-944-133-33
; Sequence 33, Application US/08944133
; Patent No. 5789542
;  GENERAL INFORMATION:
;     APPLICANT:  McLaughlin, Mark L
;     APPLICANT:  Becker, Calvin L
;     TITLE OF INVENTION:  Amphipathic Peptides
;     NUMBER OF SEQUENCES:  54
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  John H. Runnels
;       STREET:  P. O. Box 2471
;       CITY:  Baton Rouge
;       STATE:  LA
;       COUNTRY:  USA
;       ZIP:  70821-2471
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/944,133
;       FILING DATE:  06-OCT-1997
;       CLASSIFICATION:  5530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/789,077
;       FILING DATE:  03-FEB-1997
;       APPLICATION NUMBER:  US/08/681,075
;       FILING DATE:
;       APPLICATION NUMBER:  US/09/232,525
;       FILING DATE:  22-APR-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Runnels, John H
;       REGISTRATION NUMBER:  33451
;       REFERENCE/DOCKET NUMBER:  Atty File No. 5789542 9301
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  504 387-4221
;       TELEFAX:  504 346-8049
;   INFORMATION FOR SEQ ID NO:  33:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  14 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
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US-08-944-133-33

  Query Match             75.8%;  Score 50;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 0.19;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 KALKALLEKALKAL 15
              |||||| ||||||
Db          2 KALKALKKALKAL 14


RESULT 7
US-08-944-133-17
; Sequence 17, Application US/08944133
; Patent No. 5789542
;  GENERAL INFORMATION:
;    APPLICANT:  McLaughlin, Mark L.
;    APPLICANT:  Becker, Calvin L.
;    TITLE OF INVENTION:  Amphipathic Peptides
;    NUMBER OF SEQUENCES:  54
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  John H. Runnels
;      STREET:  P. O. Box 2471
;      CITY:  Baton Rouge
;      STATE:  LA
;      COUNTRY:  USA
;      ZIP:  70821 2471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/944,133
;      FILING DATE:  06-OCT-1997
;      CLASSIFICATION:  5530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/789,077
;      FILING DATE:  03-FEB-1997
;      APPLICATION NUMBER:  US/08/681,075
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/232,525
;      FILING DATE:  22-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Runnels, John H.
;      REGISTRATION NUMBER:  33451
;      REFERENCE/DOCKET NUMBER:  Atty File No. 5789542 9301
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  504 387-3221
;      TELEFAX:  504 346-8049
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-944-133-17

  Query Match             75.8%;  Score 50;  DB 1;  Length 21;
  Best Local Similarity   92.3%;  Pred. No. 0.28;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 KALKALLEKALKAL 15
              |||||| ||||||
Db          1 KALKALKKALKAL 13


RESULT 8
US-08-944-133-30
; Sequence 30, Application US/08944133
; Patent No. 5789542
;  GENERAL INFORMATION:
;    APPLICANT:  McLaughlin, Mark L.
;    APPLICANT:  Becker, Calvin L.
;    TITLE OF INVENTION:  Amphipathic Peptides
;    NUMBER OF SEQUENCES:  54
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  John H. Runnels
;      STREET:  P. O. Box 2471
;      CITY:  Baton Rouge
;      STATE:  LA
;      COUNTRY:  USA
;      ZIP:  70821 2471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/944,133
;      FILING DATE:  06-OCT-1997
;      CLASSIFICATION:  5530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/789,077
;      FILING DATE:  03-FEB-1997
;      APPLICATION NUMBER:  US/08/681,075
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/232,525
;      FILING DATE:  22-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Runnels, John H.
;      REGISTRATION NUMBER:  33451
;      REFERENCE/DOCKET NUMBER:  Atty File No. 5789542 9301
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  504 387-3221
;      TELEFAX:  504 346-8049
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-944-133-30

  Query Match             75.8%;  Score 50;  DB 1;  Length 21;
  Best Local Similarity   92.3%;  Pred. No. 0.28;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 KALKALLEKALKAL 15
              |||||| ||||||
Db          9 KALKALKKALKAL 17


RESULT 9
US-08-944-133-34
; Sequence 34, Application US/08944133
; Patent No. 5789542
;  GENERAL INFORMATION:
;    APPLICANT:  McLaughlin, Mark L.
;    APPLICANT:  Becker, Calvin L.
;    TITLE OF INVENTION:  Amphipathic Peptides
;    NUMBER OF SEQUENCES:  54
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  John H. Runnels
;      STREET:  P. O. Box 2471
;      CITY:  Baton Rouge
;      STATE:  LA
;      COUNTRY:  USA
;      ZIP:  70821 2471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
```

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;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  [illegible]/544,133
;       FILING DATE:  06-OCT-1997
;       CLASSIFICATION:  5530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/789,077
;       FILING DATE:  03-FEB-1997
;       APPLICATION NUMBER:  US/08/681,075
;       FILING DATE:
;       APPLICATION NUMBER:  US/08/222,525
;       FILING DATE:  22-APR-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Runnels, John H
;       REGISTRATION NUMBER:  33451
;       REFERENCE/DOCKET NUMBER:  Atty File No  5789542 9301
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  504 387 3221
;       TELEFAX:  504 346-8049
;   INFORMATION FOR SEQ ID NO:  34:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  21 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-944-133-34

  Query Match             75.8%;  Score 50;  DB 1;  Length 21;
  Best Local Similarity   92.3%;  Pred. No. 0.28;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 KALKALLKALKAL 15
              ||||||  ||||||
Db          2 KALKALKKALKAL 14


RESULT 10
US-08-231-730A-39
; Sequence 39, Application US/08231730A
; Patent No. 5561107
;  GENERAL INFORMATION:
;    APPLICANT:  JAYNES, JESSE M.
;    APPLICANT:  JULIAN, GORDON R.
;    TITLE OF INVENTION:  METHOD OF ENHANCING WOUND HEALING BY STIMULATING FIBROBLAST AN
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STEVEN J. HULTQUIST
;      ADDRESSEE:  INTELLECTUAL PROPERTY/TECHNOLOGY LAW
;      STREET:  200 PARK DRIVE, SUITE 210
;      STREET:  P.O. BOX 14329
;      CITY:  RESEARCH TRIANGLE PARK
;      STATE:  NORTH CAROLINA
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.4 MB STORAGE
;      COMPUTER:  APPLE MACINTOSH
;      OPERATING SYSTEM:  MACINTOSH
;      SOFTWARE:  M.S. WORD 5.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/231,730A
;      FILING DATE:  04-20-94
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/225,476
;      FILING DATE:  04-08-94
;      APPLICATION NUMBER:  08/039,620
;      FILING DATE:  06-04-93
;      APPLICATION NUMBER:  08/148,491
;      FILING DATE:  11-08-93
;      APPLICATION NUMBER:  08/148,889
;      FILING DATE:  11-08-93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HULTQUIST, STEVEN J.
;      REGISTRATION NUMBER:  28021
;      REFERENCE/DOCKET NUMBER:  4313-106
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919)990-9531
;      TELEFAX:  (919)990-9532
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23
;      TYPE:  AMINO ACID
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:
;      DESCRIPTION:  PEPTIDE
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:  COMPLETE PEPTIDE
;    ORIGINAL SOURCE:  SYNTHETIC
;    IMMEDIATE SOURCE:  SYNTHETIC
;    PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
US-08-231-730A-39

  Query Match             72.7%;  Score 48;  DB 1;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 11
US-08-427-001C-44
; Sequence 44, Application US/08427001C
; Patent No. 5717064
;  GENERAL INFORMATION:
;    APPLICANT:  JULIAN, GORDON R.
;    TITLE OF INVENTION:  METHYLATED LYSINE-RICH LYTIC PEPTIDES,
;    TITLE OF INVENTION:  AND METHODS OF MAKING THE SAME BY RECOMBINATIVE ALKYLATION
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
;      STREET:  555 Thirteenth Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.4 MB STORAGE
;      COMPUTER:  IBM COMPATIBLE
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/427,001C
;      FILING DATE:  24-APR-95
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S.08/148,889
;      FILING DATE:  08-NOV-93
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WALKER, BARBARA W.
;      REGISTRATION NUMBER:  35,400
;      REFERENCE/DOCKET NUMBER:  2093 105A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)783 6040
;      TELEFAX:  (202)783-6031
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23
;      TYPE:  AMINO ACID
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PEPTIDE
US-08-427-001C-44

  Query Match             72.7%;  Score 48;  DB 1;  Length 23;
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  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 12
US-08-457-171-39
; Sequence 39, Application US/08457171
; Patent No. 5774413
;  GENERAL INFORMATION:
;    APPLICANT:  JAYNES, JESSE M.
;    APPLICANT:  JULIAN, GORDON R.
;    TITLE OF INVENTION:  METHOD OF COMBATTING MAMMALIAN NEOPLASIA, AND LYTIC PEPTIDES I
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STEVEN J. HULTQUIST
;      ADDRESSEE:  INTELLECTUAL PROPERTY/TECHNOLOGY LAW
;      STREET:  200 PARK DRIVE, SUITE 210
;      STREET:  P.O. BOX 14329
;      CITY:  RESEARCH TRIANGLE PARK
;      STATE:  NORTH CAROLINA
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.4 MB STORAGE
;      COMPUTER:  APPLE MACINTOSH
;      OPERATING SYSTEM:  MACINTOSH
;      SOFTWARE:  M.S. WORD 5.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,171
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/225,476A
;      FILING DATE:  04-08-94
;      APPLICATION NUMBER:  08/039,620
;      FILING DATE:  06-04-93
;      APPLICATION NUMBER:  08/148,491
;      FILING DATE:  11-08-93
;      APPLICATION NUMBER:  08/148,889
;      FILING DATE:  11-08-93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HULTQUIST, STEVEN J.
;      REGISTRATION NUMBER:  28021
;      REFERENCE/DOCKET NUMBER:  4013-106
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919)990-9531
;      TELEFAX:  (919)990-9532
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23
;      TYPE:  AMINO ACID
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:
;      DESCRIPTION:  PEPTIDE
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:  COMPLETE PEPTIDE
;    ORIGINAL SOURCE:  SYNTHETIC
;    IMMEDIATE SOURCE:  SYNTHETIC
;    PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
US-08-457-171-39

  Query Match             72.7%;  Score 48;  DB 1;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 13
US-08-723-306-19
; Sequence 19, Application US/08723306
; Patent No. 5856178
;  GENERAL INFORMATION:
;    APPLICANT:  White PhD, Kenneth
;    APPLICANT:  Murrey PhD, John
;    APPLICANT:  Reed, William
;    TITLE OF INVENTION:  Cassette for Expression [illegible]
;    TITLE OF INVENTION:  Peptides in Mammalian Hosts [illegible]
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Trask Britt and Rossa
;      STREET:  P.O. Box 2550
;      CITY:  Salt Lake City
;      STATE:  Utah
;      COUNTRY:  USA
;      ZIP:  84110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #[illegible]
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/723,306
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sweigart PhD, Susan E
;      REGISTRATION NUMBER:  38,486
;      REFERENCE/DOCKET NUMBER:  2740
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  8015321922
;      TELEFAX:  8015329168
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  No
US-08-723-306-19

  Query Match             72.7%;  Score 48;  DB [illegible]  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 14
US-08-505-486-44
; Sequence 44, Application US/08505486
; Patent No. 5955573
;  GENERAL INFORMATION:
;    APPLICANT:  Jesse M. Jaynes
;    TITLE OF INVENTION:  Oligolin Lytic Peptide [illegible] N-Myc
;    TITLE OF INVENTION:  Constructs, Protein Products Thereof, Cells M. An
;    TITLE OF INVENTION:  Methods of Making and Using Same
;    NUMBER OF SEQUENCES:  98
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BOTHWELL, FISH, ERNST & KUEZ
;      STREET:  555 Thirteenth Street N.W.
;      CITY:  Washington
;      STATE:  D. C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.4 MB [illegible]
```

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;       COMPUTER:  IBM COMPATIBLE
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  WordPerfect 5.1+
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/505,486
;       FILING DATE:  21-JUL-1995
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  U.S. 08/279,472
;       FILING DATE:  22-JUL-1994
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WALKER, BARBARA W.
;       REGISTRATION NUMBER:  35,400
;       REFERENCE/DOCKET NUMBER:  2093-117A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)783-6040
;       TELEFAX:  (202)783-6031
;   INFORMATION FOR SEQ ID NO:  44:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:
;       DESCRIPTION:  PEPTIDE
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  COMPLETE PEPTIDE
;     ORIGINAL SOURCE:  SYNTHETIC
;     IMMEDIATE SOURCE:  SYNTHETIC
;     PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
US 08-505 486-44

  Query Match             72.7%;  Score 48;  DB 2;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALEKALKEL 15


RESULT 15
US-08 689-489C-39
; Sequence 39, Application US/08689489C
; Patent No. 6001805
;  GENERAL INFORMATION:
;     APPLICANT:  Jesse M. Jaynes, Gordon R. Julian
;     TITLE OF INVENTION:  Method of Enhancing Wound Healing By
;     TITLE OF INVENTION:  Stimulating Fibro-blast and Keratinocyte Growth In
;     TITLE OF INVENTION:  Vivo, Utilizing Amphipathic Peptides
;     NUMBER OF SEQUENCES:  46
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Rothwell, Figg, Ernst & Kurz
;       STREET:  555 13TH STREET
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/689,489C
;       FILING DATE:  August 12, 1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/231,730
;       FILING DATE:  April 20, 1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/225,476
;       FILING DATE:  April 8, 1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/039,620
;       FILING DATE:  June 4, 1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/148,889
;       FILING DATE:  No. 6001805ember 8, 1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/148,491
;       FILING DATE:  No. 6001805ember 8, 1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Mark L. Bowditch
;       REGISTRATION NUMBER:  40,315
;       REFERENCE/DOCKET NUMBER:  2093-120
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-783-6040
;       TELEFAX:  202-783 6031
;   INFORMATION FOR SEQ ID NO:  39:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  linear
US-08-689-489C-39

  Query Match             72.7%;  Score 48;  DB 3;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALEKALKEL 15


RESULT 16
US-08-801-028 44
; Sequence 44, Application US/08801028
; Patent No. 6018102
;  GENERAL INFORMATION:
;     APPLICANT:  JOAN GARBARINO
;     APPLICANT:  JESSE M. JAYNES
;     APPLICANT:  WILLIAM BELKNAP
;     TITLE OF INVENTION:  UBIQUITIN LYTIC PEPTIDE FUSION GENE CONSTRUCTS, EXPRESSION
;     NUMBER OF SEQUENCES:  98
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  STEVEN J. HULTQUIST
;       ADDRESSEE:  INTELLECTUAL PROPERTY/TECHNOLOGY LAW
;       STREET:  200 PARK DRIVE, SUITE 210
;       STREET:  P.O. BOX 14329
;       CITY:  RESEARCH TRIANGLE PARK
;       STATE:  NORTH CAROLINA
;       COUNTRY:  USA
;       ZIP:  27709
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.4 MB STORAGE
;       COMPUTER:  APPLE MACINTOSH
;       OPERATING SYSTEM:  MACINTOSH
;       SOFTWARE:  M.S. WORD 5.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/801,028
;       FILING DATE:  19 FEB-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/279,472
;       FILING DATE:  JULY 22, 1994
;       APPLICATION NUMBER:  08/225,476
;       FILING DATE:  04-20 94
;       APPLICATION NUMBER:  08/225,476
;       FILING DATE:  04-08-94
;       APPLICATION NUMBER:  08/039,620
;       FILING DATE:  06 04-93
;       APPLICATION NUMBER:  08/148,491
;       FILING DATE:  11 08-93
```

```
;       APPLICATION NUMBER:  08/148,889
;       FILING DATE:  11-08-93
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WASSERMAN, FRAN S.
;       REGISTRATION NUMBER:  34,273
;       REFERENCE/DOCKET NUMBER:  4013 104
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (919)990-9531
;       TELEFAX:  (919)990-9532
;   INFORMATION FOR SEQ ID NO:  44:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:
;       DESCRIPTION:  PEPTIDE
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  COMPLETE PEPTIDE
;     ORIGINAL SOURCE:  SYNTHETIC
;     IMMEDIATE SOURCE:  SYNTHETIC
;     PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
US-08-801-028-44

  Query Match             72.7%;  Score 48;  DB 4;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 17
US-09-340-154-44
; Sequence 44, Application US/09340154
; Patent No. 6084156
;  GENERAL INFORMATION:
;     APPLICANT:  Jesse M. Jaynes
;     TITLE OF INVENTION:  UBIQUITIN-LYTIC PEPTIDE FUSION GENE
;     TITLE OF INVENTION:  CONSTRUCTS, PROTEIN PRODUCTS DERIVING THEREFROM, AND
;     TITLE OF INVENTION:  METHODS OF MAKING AND USING SAME
;     NUMBER OF SEQUENCES:  98
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
;       STREET:  555 Thirteenth Street N.W.
;       CITY:  Washington
;       STATE:  D. C.
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 5.5 INCH, 1.4 MB STORAGE
;       COMPUTER:  IBM COMPATIBLE
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  WordPerfect 5.1+
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  08/[illegible]
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/505,480
;       FILING DATE:  21-JUL-1995
;       APPLICATION NUMBER:  U.S. 08/279,472
;       FILING DATE:  22 JUL-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WALKER, BARBARA W.
;       REGISTRATION NUMBER:  [illegible]
;       REFERENCE/DOCKET NUMBER:  2099.117A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)783-6040
;       TELEFAX:  (202)783-6031
;   INFORMATION FOR SEQ ID NO:  44:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:
;       DESCRIPTION:  PEPTIDE
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  COMPLETE PEPTIDE
;     ORIGINAL SOURCE:  SYNTHETIC
;     IMMEDIATE SOURCE:  SYNTHETIC
;     PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
US-09-340-154-44

  Query Match             72.7%;  Score 48;  DB 4;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 18
US-09-242-802A-59
; Sequence 59, Application US/09242802A
; Patent No. 6191110
;   GENERAL INFORMATION:
;       APPLICANT: Jesse M. Jaynes, Gordon R. Julian
;       TITLE OF INVENTION: Method of Enhancing Wound Healing by
;                           Stimulation Fibroblast Proliferation with Synthetic
;                           Virus Derived Amphipathic Peptides
;       NUMBER OF SEQUENCES: 46
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Rothwell, Figg, Ernst & Manbeck
;            STREET: 555 13th STREET
;            CITY: Washington
;            STATE: DC
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/242,802A
;            FILING DATE: 19 Jan 1999
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/689,480
;            FILING DATE: August 12, 1996
;            APPLICATION NUMBER: US 08/279,472
;            FILING DATE: April 29, 1994
;            APPLICATION NUMBER: US 08/235,417
;            FILING DATE: April 8, 1994
;            APPLICATION NUMBER: US 08/039,620
;            FILING DATE: June 4, 1993
;            APPLICATION NUMBER: 08/148,889
;            FILING DATE: Nov. 8 [illegible]ember 8, 1993
;            APPLICATION NUMBER: 08/148,401
;            FILING DATE: Nov. 8 [illegible]ember 8, 1993
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Mark J. Bowditch
;            REGISTRATION NUMBER: 44,415
;            REFERENCE/DOCKET NUMBER: 2099.117
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202 783 6040
;            TELEFAX: 202 783 6031
;   INFORMATION FOR SEQ ID NO: 59:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 23 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: Unknown
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       HYPOTHETICAL: NO
```

```
;          FRAGMENT TYPE: Linear
;          SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-232-802A-39

  Query Match             72.7%;  Score 48;  DB 3;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 19
US-09-482-611B-44
; Sequence 44, Application US/09482611B
; Patent No. 6448391
; GENERAL INFORMATION:
;  APPLICANT: Garbarino, Joan
;  APPLICANT:  Belknap, William
;  TITLE OF INVENTION: Ubiquitin-Lytic Peptide Fusion Gene Constructs, Protein Products
;  TITLE OF INVENTION:  Therefrom, and Methods of Making and Using Same
;  FILE REFERENCE: 2093-149
;  CURRENT APPLICATION NUMBER: US/09/482,611B
;  CURRENT FILING DATE:  2000-01-14
;  PRIOR APPLICATION NUMBER: US 08/801,028
;  PRIOR FILING DATE: 1997-02-19
;  PRIOR APPLICATION NUMBER: US 08/279,473
;  PRIOR FILING DATE: 1994-07-22
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: Patentin version 3.1
; SEQ ID NO 44
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Lytic Peptide
US-09-482-611B-44

  Query Match             72.7%;  Score 48;  DB 4;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 20
US-09-019-922A-44
; Sequence 44, Application US/09019922A
; Patent No. 6559281
;  GENERAL INFORMATION:
;     APPLICANT:  JAYNES, JESSE M.
;     TITLE OF INVENTION:  NON NATURALLY OCCURRING SYNTHETIC LYTIC
;     TITLE OF INVENTION:  PEPTIDES
;     NUMBER OF SEQUENCES:  45
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  ROTHWELL, FIGG, ERNST & MANBECK
;       STREET:  555 Thirteenth Street, N.W.
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.4 MB STORAGE
;       COMPUTER:  IBM COMPATIBLE
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  WordPad
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/019,922A
;       FILING DATE:  06-FEB-98
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  U.S.08/427,001
;       FILING DATE:  24-APR-95
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  U.S.08/148,889
;       FILING DATE:  08-NOV-93
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BOWDITCH, MARK I.
;       REGISTRATION NUMBER:  40,415
;       REFERENCE/DOCKET NUMBER:  2093-153A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)783-6040
;       TELEFAX:  (202)783-6041
;   INFORMATION FOR SEQ ID NO:  44:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:  PEPTIDE
US-09-019-922A-44

  Query Match             72.7%;  Score 48;  DB 4;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 21
PCT US94-12550-47
; Sequence 47, Application PC/TUS9412550
;  GENERAL INFORMATION:
;     APPLICANT:  JULIAN, GORDON R.
;     TITLE OF INVENTION:  METHYLATED LYSINE RICH LYTIC
;     TITLE OF INVENTION:  PEPTIDES AND METHOD OF
;     TITLE OF INVENTION:  MAKING SAME BY REDUCTIVE
;     TITLE OF INVENTION:  ALKYLATION
;     NUMBER OF SEQUENCES:  47
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  STEVEN J. HULTQUIST
;       ADDRESSEE:  INTELLECTUAL PROPERTY/TECHNOLOGY LAW
;       STREET:  200 PARK DRIVE, SUITE 210
;       STREET:  P.O. BOX 14329
;       CITY:  RESEARCH TRIANGLE PARK
;       STATE:  NORTH CAROLINA
;       COUNTRY:  USA
;       ZIP:  27709
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 5.5 INCH, 1.4 MB STORAGE
;       COMPUTER:  APPLE MACINTOSH
;       OPERATING SYSTEM:  MACINTOSH
;       SOFTWARE:  M.S. WORD 5.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PC/US94/12550
;       FILING DATE:  NOVEMBER 8, 1994
;     PRIOR APPLICATION DATA:  NONE
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  HULTQUIST, STEVEN J.
;       REGISTRATION NUMBER:  28021
;       REFERENCE/DOCKET NUMBER:  4013.101
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (919)990-9531
;       TELEFAX:  (919)990-9532
;   INFORMATION FOR SEQ ID NO:  47:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:
;       DESCRIPTION:  PEPTIDE
;     HYPOTHETICAL:  NO
```

```
;     FRAGMENT TYPE:  COMPLETE PEPTIDE
;     ORIGINAL SOURCE:  SYNTHETIC
;     IMMEDIATE SOURCE:  SYNTHETIC
PCT-US94-12550-47

  Query Match             72.7%;  Score 48;  DB 5;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 22
PCT-US95-04435-39
; Sequence 39, Application PC/TUS9504435
;  GENERAL INFORMATION:
;     APPLICANT:  JAYNES, JESSE M.
;     APPLICANT:  JULIAN, GORDON R.
;     TITLE OF INVENTION:  METHOD OF COMBATTING MAMMALIAN NEOPLASIA, AND LYTIC PEPTIDES T
;     NUMBER OF SEQUENCES:  40
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  FRAN S. WASSERMAN
;       ADDRESSEE:  INTELLECTUAL PROPERTY/TECHNOLOGY LAW
;       STREET:  200 PARK DRIVE, SUITE 210
;       STREET:  P.O. BOX 14329
;       CITY:  RESEARCH TRIANGLE PARK
;       STATE:  NORTH CAROLINA
;       COUNTRY:  USA
;       ZIP:  27709
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.4 MB STORAGE
;       COMPUTER:  APPLE MACINTOSH
;       OPERATING SYSTEM:  MACINTOSH
;       SOFTWARE:  M.S. WORD 6.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/04435
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USA08/225,476
;       FILING DATE:  04-08-94
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WASSERMAN, FRAN S.
;       REGISTRATION NUMBER:  34273
;       REFERENCE/DOCKET NUMBER:  4013-106PCT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (919)990-9531
;       TELEFAX:  (919)990-9532
;   INFORMATION FOR SEQ ID NO:  39:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:
;       DESCRIPTION:  PEPTIDE
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  COMPLETE PEPTIDE
;     ORIGINAL SOURCE:  SYNTHETIC
;     IMMEDIATE SOURCE:  SYNTHETIC
;     PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
PCT-US95-04435-39

  Query Match             72.7%;  Score 48;  DB 5;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 23
```

```
PCT-US95-04718-39
; Sequence 39, Application PC/TUS9504718
;  GENERAL INFORMATION:
;     APPLICANT:  DEMETER BIOTECHNOLOGIES, LTD.
;     TITLE OF INVENTION:  METHOD OF ENHANCING WOUND HEALING BY ADMINISTRATION OF A
;     NUMBER OF SEQUENCES:  46
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  FRAN S. WASSERMAN
;       ADDRESSEE:  INTELLECTUAL PROPERTY/TECHNOLOGY LAW
;       STREET:  200 PARK DRIVE, SUITE 210
;       STREET:  P.O. BOX 14329
;       CITY:  RESEARCH TRIANGLE PARK
;       STATE:  NORTH CAROLINA
;       COUNTRY:  USA
;       ZIP:  27709
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.4 MB STORAGE
;       COMPUTER:  APPLE MACINTOSH
;       OPERATING SYSTEM:  MACINTOSH
;       SOFTWARE:  M.S. WORD 6.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/04718
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/231,730
;       FILING DATE:  20-04-94
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WASSERMAN, FRAN S.
;       REGISTRATION NUMBER:  34273
;       REFERENCE/DOCKET NUMBER:  4013-107
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (919)990-9531
;       TELEFAX:  (919)990-9532
;   INFORMATION FOR SEQ ID NO:  39:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:
;       DESCRIPTION:  PEPTIDE
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  COMPLETE PEPTIDE
;     ORIGINAL SOURCE:  SYNTHETIC
;     IMMEDIATE SOURCE:  SYNTHETIC
;     PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
PCT-US95-04718-39

  Query Match             72.7%;  Score 48;  DB 5;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 24
PCT-US95-09338-44
; Sequence 44, Application PC/TUS9509338
;  GENERAL INFORMATION:
;     APPLICANT:
;     TITLE OF INVENTION:  SYNTHETIC LYTIC PEPTIDE E-C-C-N-TERMI
;     TITLE OF INVENTION:  CONSTRUCTS, PROTEIN PRODUCTS DERIVING THEREFROM, AND
;     TITLE OF INVENTION:  METHODS OF MAKING AND USING THE SAME
;     NUMBER OF SEQUENCES:  98
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/09338
;       FILING DATE:  21-JUL-1994
```

```
;     PRIOR APPLICATION DATA:  08/279,472
;       APPLICATION NUMBER:  08/279,472
;       FILING DATE:  22-JUL-1994
;   INFORMATION FOR SEQ ID NO:  44:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:
;       DESCRIPTION:  PEPTIDE
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  COMPLETE PEPTIDE
;     ORIGINAL SOURCE:  SYNTHETIC
;     IMMEDIATE SOURCE:  SYNTHETIC
;     PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
PCT-US95-09338-44

  Query Match             72.7%;  Score 48;  DB 5;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 25
PCT-US95-09339-44
; Sequence 44, Application PC/TUS9509339
;  GENERAL INFORMATION:
;     APPLICANT:
;     APPLICANT:
;     TITLE OF INVENTION:  UBIQUITIN-LYTIC PEPTIDE FUSION GENE
;     TITLE OF INVENTION:  CONSTRUCTS, PROTEIN PRODUCTS DERIVING THEREFROM, AND
;     TITLE OF INVENTION:  METHODS OF MAKING AND USING THE SAME
;     NUMBER OF SEQUENCES:  98
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WORDPERFECT 5.1+
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/09339
;       FILING DATE:  21-JUL-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/279,472
;       FILING DATE:  22-JUL-1994
;   INFORMATION FOR SEQ ID NO:  44:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:
;       DESCRIPTION:  PEPTIDE
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  COMPLETE PEPTIDE
;     ORIGINAL SOURCE:  SYNTHETIC
;     IMMEDIATE SOURCE:  SYNTHETIC
;     PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
PCT-US95-09339-44

  Query Match             72.7%;  Score 48;  DB 5;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 26
PCT-US96-10041-19
; Sequence 19, Application PC/TUS9610041

;  GENERAL INFORMATION:
;     APPLICANT:  White PhD, Kenneth
;     APPLICANT:  Morrey PhD, John
;     APPLICANT:  Rood, William
;     TITLE OF INVENTION:  Cassette for Expression of Lytic
;     TITLE OF INVENTION:  Peptides in Mammalian Transgenic Organisms
;     NUMBER OF SEQUENCES:  32
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Trask Britt and Rossa
;       STREET:  P.O. Box 2550
;       CITY:  Salt Lake City
;       STATE:  Utah
;       COUNTRY:  USA
;       ZIP:  84110
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  Patentin Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US96/10041
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Swoiqert PhD, Susan E
;       REGISTRATION NUMBER:  35,299
;       REFERENCE/DOCKET NUMBER:  2549
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  8015321922
;       TELEFAX:  8015319168
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  YES
;     ANTI-SENSE:  NO
PCT-US96-10041-19

  Query Match             72.7%;  Score 48;  DB 5;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.58;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 27
US-07-908-455A-8
; Sequence 8, Application US/07908455A
; Patent No. 5459237
;  GENERAL INFORMATION:
;     APPLICANT:  Berkowitz, Barry A.
;     APPLICANT:  Kari, U. Prasad
;     APPLICANT:  Maloy, W. Lee
;     TITLE OF INVENTION:  No. 5459237ol Peptide Compositions and
;     TITLE OF INVENTION:  Uses Therefor
;     NUMBER OF SEQUENCES:  89
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Carella, Byrne, Bain, Gilfillan
;       ADDRESSEE:  Cecchi & Stewart
;       STREET:  6 Becker Farm Road
;       CITY:  Roseland
;       STATE:  New Jersey
;       COUNTRY:  USA
;       ZIP:  07068
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5 inch diskette
;       COMPUTER:  IBM PS/2
;       OPERATING SYSTEM:  PC-DOS
```

```
;       SOFTWARE:  DW4.V2
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/909,455A
;       FILING DATE:  19920702
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07686115
;       FILING DATE:  15 APR 1991
;       APPLICATION NUMBER:  US 07476629
;       FILING DATE:  08 FEB 1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Olstein, Elliot M.
;       REGISTRATION NUMBER:  24,025
;       REFERENCE/DOCKET NUMBER:  421250-122
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-994-1700
;       TELEFAX:  201-994-1744
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  21 amino acids
;       TYPE:  AMINO ACID
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       OTHER INFORMATION:  amido terminated
US-07-908-455A-8

  Query Match             60.6%;  Score 40;  DB 1;  Length 21;
  Best Local Similarity   61.5%;  Prod. No. 7.3;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           3 KAIKAIIKAIKAI 15
               |:|:|: ||:||
Db           5 KAIKAIGKAIKAI 17


RESULT 28
US-08-434-120-34
; Sequence 34, Application US/08421120
; Patent No. 5635479
;  GENERAL INFORMATION:
;     APPLICANT:  Baker, Margaret A.
;     APPLICANT:  Jacob, Leonard S.
;     APPLICANT:  Maloy, W. Lee
;     TITLE OF INVENTION:  Treatment of Gynecological
;     TITLE OF INVENTION:  Malignancies with
;     TITLE OF INVENTION:  Biologically Active Peptides
;     NUMBER OF SEQUENCES:  117
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;       ADDRESSEE:  Cecchi & Stewart
;       STREET:  6 Becker Farm Road
;       CITY:  Roseland
;       STATE:  New Jersey
;       COUNTRY:  USA
;       ZIP:  07068
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5 inch diskette
;       COMPUTER:  IBM PS/2
;       OPERATING SYSTEM:  PC-DOS
;       SOFTWARE:  DW4.V2
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/141,123
;       FILING DATE:
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/257,950
;       FILING DATE:
;       APPLICATION NUMBER:  US/08/226,108
;       FILING DATE:
;       APPLICATION NUMBER:  US/07/637,462
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Olstein, Elliot M.
;       REGISTRATION NUMBER:  24,025
;       REFERENCE/DOCKET NUMBER:  421250-194
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201 994 1700
;       TELEFAX:  201 994 1744
;   INFORMATION FOR SEQ ID NO:  34:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  21 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-434-120-34

  Query Match             60.6%;  Score 40;  DB 1;  Length 21;
  Best Local Similarity   61.5%;  Prod. No. 7.3;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           3 KAIKAIIKAIKAI 15
               |:|:|: ||:||
Db           5 KAIKAIGKAIKAI 17


RESULT 29
US-08-465-325-34
; Sequence 34, Application US/08465325
; Patent No. 5686563
;  GENERAL INFORMATION:
;     APPLICANT:  Magainin Pharmaceuticals Inc.
;     APPLICANT:  5110 Campus Drive
;     APPLICANT:  Plymouth Meeting, PA  19462
;     TITLE OF INVENTION:  Biologically Active Peptides
;     TITLE OF INVENTION:  N-Terminal Substitutions
;     NUMBER OF SEQUENCES:  154
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;       ADDRESSEE:  Dunner
;       STREET:  1300 I Street, N.W. Suite 700
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20005-3315
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.3
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  08/465,325
;       FILING DATE:  05 JUN 1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/184,469
;       FILING DATE:  18 JAN 94
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/990,760
;       FILING DATE:  01 JUN 92
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Fordis, Jean B.
;       REGISTRATION NUMBER:  32,984
;       REFERENCE/DOCKET NUMBER:  00 0925 0021 00
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 408 4000
;       TELEFAX:  (202) 408 4400
;   INFORMATION FOR SEQ ID NO:  34:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  21 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  linear
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-465-325-34
```

```
  Query Match             60.6%;  Score 40;  DB 1;  Length 21;
  Best Local Similarity   61.5%;  Pred. No. 7.3;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 KALKALIKALKAL 15
              ||:||: ||:||:
Db          5 KAIKAIGKAIKAI 17


RESULT 30
US-09-115-737-34
; Sequence 34, Application US/09115737
; Patent No. 6348445
;   GENERAL INFORMATION:
;        APPLICANT: G. Prasad Kari
;                   Taffy J. Williams
;                   Michael McLane
;        TITLE OF INVENTION: Biologically Active Peptides With Reduced
;                            Toxicity in Animals and a Method for Preparing Same
;        NUMBER OF SEQUENCES: 156
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
;                        Dunner, L.L.P.
;             STREET: 1300 I Street, N.W. Suite 700
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20005-3315
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.3
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/115,737
;             FILING DATE: 15-Jul-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/465,330
;             FILING DATE: 05-JUN-1995
;             APPLICATION NUMBER: 08/184,462
;             FILING DATE: 18-JAN-94
;             APPLICATION NUMBER: 07/891,201
;             FILING DATE: 01-JUN-92
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fordis, Joan B
;             REGISTRATION NUMBER: 32,984
;             REFERENCE/DOCKET NUMBER: 05487.0021-00000
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 408-4000
;             TELEFAX: (202) 408-4400
;   INFORMATION FOR SEQ ID NO: 34:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 21 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-115-737-34

  Query Match             60.6%;  Score 40;  DB 4;  Length 21;
  Best Local Similarity   61.5%;  Pred. No. 7.3;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 KALKALIKALKAL 15
              ||:||: ||:||:
Db          5 KAIKAIGKAIKAI 17


RESULT 31
US-08-752-526-3
; Sequence 3, Application US/08752526
; Patent No. 6124429
;   GENERAL INFORMATION:
;     APPLICANT:  Miura et al., Kin-ichiro
;     TITLE OF INVENTION:  POLYPEPTIDE
;     NUMBER OF SEQUENCES:  13
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fish & Richardson P.C.
;       STREET:  601 Thirteenth Street, NW
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/752,526
;       FILING DATE:  20-NOV-1996
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP H 08 112128
;       FILING DATE:  10-APR-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ellison, Eldora L.
;       REGISTRATION NUMBER:  39,967
;       REFERENCE/DOCKET NUMBER:  07316/022001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202/783-5070
;       TELEFAX:  202/783-2331
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  22 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-752-526-3

  Query Match             59.1%;  Score 39;  DB 4;  Length 22;
  Best Local Similarity   64.3%;  Pred. No. 11;
  Matches    9;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 AKALKALLKALKAL 16
              |:||: | |||: |
Db          6 AKALETLAKALEIL 19


RESULT 42
US-08-231-730A-42
; Sequence 42, Application US/08231730A
; Patent No. 5561107
;   GENERAL INFORMATION:
;     APPLICANT:  JAYNES, JESSE M.
;     APPLICANT:  JULIAN, GORDON R.
;     TITLE OF INVENTION:  METHOD OF ENHANCING WOUND HEALING BY STIMULATING FIBR
;     NUMBER OF SEQUENCES:  46
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  STEVEN J. HULTQUIST
;       ADDRESSEE:  INTELLECTUAL PROPERTY/TECHNOLOGY LAW
;       STREET:  200 PARK DRIVE, SUITE 210
;       STREET:  P.O. BOX 14329
;       CITY:  RESEARCH TRIANGLE PARK
;       STATE:  NORTH CAROLINA
;       COUNTRY:  USA
;       ZIP:  27709
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 5.0 INCH, 1.4 MB STORAGE
;       COMPUTER:  APPLE MACINTOSH
;       OPERATING SYSTEM:  MACINTOSH
;       SOFTWARE:  M.S. WORD 5.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/231,730A
```

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;       FILING DATE:  04-20-94
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/225,476
;       FILING DATE:  04-08-94
;       APPLICATION NUMBER:  08/139,620
;       FILING DATE:  06-04-93
;       APPLICATION NUMBER:  08/148,491
;       FILING DATE:  11-08-93
;       APPLICATION NUMBER:  08/148,889
;       FILING DATE:  11-08-93
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  HULTQUIST, STEVEN J.
;       REGISTRATION NUMBER:  28021
;       REFERENCE/DOCKET NUMBER:  401.106
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (919)990-9531
;       TELEFAX:  (919)990-9532
;   INFORMATION FOR SEQ ID NO:  42:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:
;       DESCRIPTION:  PEPTIDE
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  COMPLETE PEPTIDE
;     ORIGINAL SOURCE:  SYNTHETIC
;     IMMEDIATE SOURCE:  SYNTHETIC
;     PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
US-08-241-730A-42

  Query Match             59.1%;  Score 39;  DB 1;  Length 23;
  Best Local Similarity   58.3%;  Pred. No. 11;
  Matches    9;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |:|| |||:|:
Db          1 FAIAIKAIKKAIKKI 15


RESULT 33
US-08-505,486-47
; Sequence 47, Application US/08505486
; Patent No. 5955573
;  GENERAL INFORMATION:
;     APPLICANT:  Jesse M. Jaynes
;     TITLE OF INVENTION:  UBIQUITIN-LYTIC PEPTIDE FUSION GENE
;     TITLE OF INVENTION:  CONSTRUCTS, PROTEIN PRODUCTS DERIVING THEREFROM, AND
;     TITLE OF INVENTION:  METHODS OF MAKING AND USING SAME
;     NUMBER OF SEQUENCES:  98
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
;       STREET:  555 Thirteenth Street N.W.
;       CITY:  Washington
;       STATE:  D. C.
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.4 MB STORAGE
;       COMPUTER:  IBM COMPATIBLE
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/505,486
;       FILING DATE:  21-JUL 1995
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/279,472
;       FILING DATE:  22-JUL 1994
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WALKER, BARBARA W.
;       REGISTRATION NUMBER:  35,400
;       REFERENCE/DOCKET NUMBER:  2093.112A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)783-6040
;       TELEFAX:  (202)783-6031
;   INFORMATION FOR SEQ ID NO:  47:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:
;       DESCRIPTION:  PEPTIDE
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  COMPLETE PEPTIDE
;     ORIGINAL SOURCE:  SYNTHETIC
;     IMMEDIATE SOURCE:  SYNTHETIC
;     PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
US-08-505,486-47

  Query Match             59.1%;  Score 39;  DB 1;  Length 23;
  Best Local Similarity   58.3%;  Pred. No. 11;
  Matches    9;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |:|| |||:|:
Db          1 FAIAIKAIKKAIKKI 15


RESULT 34
US-08-689,480C-42
; Sequence 42, Application US/08689480C
; Patent No. 6001805
;  GENERAL INFORMATION:
;     APPLICANT:  Jesse M. Jaynes, Gordon E. Levin
;     TITLE OF INVENTION:  Method of Eliminating Microbial Pathogens
;     TITLE OF INVENTION:  Stimulating Fibroblast and Keratinocyte Activity
;     TITLE OF INVENTION:  Vivo, Utilizing Amphipathic Peptides
;     NUMBER OF SEQUENCES:  46
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Rothwell, Figg, Ernst & Kurz
;       STREET:  555 13TH STREET
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/689,480C
;       FILING DATE:  August 12, 199
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/233,739
;       FILING DATE:  April 20, 1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/225,476
;       FILING DATE:  April 8, 1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/253,620
;       FILING DATE:  June 4, 1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/148,889
;       FILING DATE:  No. 6001805ember 8, 1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/148,491
;       FILING DATE:  No. 6001805ember 8, 1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Mark L. Bowitz
;       REGISTRATION NUMBER:  40,355
;       REFERENCE/DOCKET NUMBER:  2093.120
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202 783 6040
```

```
;       TELEFAX:  202-783-6031
;   INFORMATION FOR SEQ ID NO:  42:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  linear
US-08-689-489C-42

  Query Match             59.1%;  Score 39;  DB 3;  Length 23;
  Best Local Similarity   53.3%;  Pred. No. 11;
  Matches    8;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |:|| |||:| :
Db          1 FAIAIKAIKKAIKKI 15


RESULT 35
US-08-801-028-47
; Sequence 47, Application US/08801028
; Patent No. 6018102
;  GENERAL INFORMATION:
;     APPLICANT:  JOAN GARBARINO
;     APPLICANT:  JESSE M. JAYNES
;     APPLICANT:  WILLIAM BELKNAP
;     TITLE OF INVENTION:  UBIQUITIN LYTIC PEPTIDE FUSION GENE CONSTRUCTS, PROTEIN PRODUC
;     NUMBER OF SEQUENCES:  98
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  STEVEN J. HULTQUIST
;       ADDRESSEE:  INTELLECTUAL PROPERTY/TECHNOLOGY LAW
;       STREET:  200 PARK DRIVE, SUITE 210
;       STREET:  P.O. BOX 14329
;       CITY:  RESEARCH TRIANGLE PARK
;       STATE:  NORTH CAROLINA
;       COUNTRY:  USA
;       ZIP:  27709
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.4 MB STORAGE
;       COMPUTER:  APPLE MACINTOSH
;       OPERATING SYSTEM:  MACINTOSH
;       SOFTWARE:  M.S. WORD 5.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/801,028
;       FILING DATE:  19-FEB-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/279,472
;       FILING DATE:  JULY 22, 1994
;       APPLICATION NUMBER:  08/225,476
;       FILING DATE:  04-20-94
;       APPLICATION NUMBER:  08/225,476
;       FILING DATE:  04-08-94
;       APPLICATION NUMBER:  08/039,620
;       FILING DATE:  06-04-93
;       APPLICATION NUMBER:  08/148,491
;       FILING DATE:  11-08-93
;       APPLICATION NUMBER:  08/148,889
;       FILING DATE:  11-08-93
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WASSERMAN, FRAN S.
;       REGISTRATION NUMBER:  34,273
;       REFERENCE/DOCKET NUMBER:  4013-104
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (919)990-9531
;       TELEFAX:  (919)990-9532
;   INFORMATION FOR SEQ ID NO:  47:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:
;       DESCRIPTION:  PEPTIDE
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  COMPLETE PEPTIDE
;     ORIGINAL SOURCE:  SYNTHETIC
;     IMMEDIATE SOURCE:  SYNTHETIC
;     PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
US-08-801-028-47

  Query Match             59.1%;  Score 39;  DB 3;  Length 23;
  Best Local Similarity   53.3%;  Pred. No. 11;
  Matches    8;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |:|| |||:| :
Db          1 FAIAIKAIKKAIKKI 15


RESULT 46
US-09-340-154-47
; Sequence 47, Application US/09340154
; Patent No. 6084156
;  GENERAL INFORMATION:
;     APPLICANT:  Jesse M. Jaynes
;     TITLE OF INVENTION:  UBIQUITIN-LYTIC PEPTIDE FUSION GENE
;     TITLE OF INVENTION:  CONSTRUCTS, PROTEIN PRODUCTS CONTAINING THEREOF, AND
;     TITLE OF INVENTION:  METHODS OF MAKING AND USING SAME
;     NUMBER OF SEQUENCES:  98
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Rothwell, Figg, Ernst & Kurz
;       STREET:  555 Thirteenth Street N.W.
;       CITY:  Washington
;       STATE:  D. C.
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.4 MB STORAGE
;       COMPUTER:  IBM COMPATIBLE
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/340,154
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/505,486
;       FILING DATE:  21-JUL-1995
;       APPLICATION NUMBER:  U.S. 08/279,472
;       FILING DATE:  22-JUL-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WALKER, BARBARA W.
;       REGISTRATION NUMBER:  35,400
;       REFERENCE/DOCKET NUMBER:  2793-117A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)783-6040
;       TELEFAX:  (202)783-6031
;   INFORMATION FOR SEQ ID NO:  47:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:
;       DESCRIPTION:  PEPTIDE
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  COMPLETE PEPTIDE
;     ORIGINAL SOURCE:  SYNTHETIC
;     IMMEDIATE SOURCE:  SYNTHETIC
;     PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
US-09-340-154-47

  Query Match             59.1%;  Score 39;  DB 3;  Length 23;
  Best Local Similarity   53.3%;  Pred. No. 11;
  Matches    8;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy          1 FAKALKALLKALKAL 15
              || |:|| ||:| :
Db          1 FAIAIKAIKKAIKKI 15


RESULT 37
US-09-232-802A-42
; Sequence 42, Application US/09232802A
; Patent No. 6191110
;   GENERAL INFORMATION:
;        APPLICANT: Jesse M. Jaynes, Gordon K. Julian
;        TITLE OF INVENTION: Method of Enhancing Wound Healing By
;                            Stimulating Fibro-blast and Keratinocyte Growth In
;                            Vivo, Utilizing Amphipathic Peptides
;        NUMBER OF SEQUENCES: 46
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Rothwell, Figg, Ernst & Manbeck
;             STREET: 555 14TH STREET
;             CITY: Washington
;             STATE: DC
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/232,802A
;             FILING DATE: 19-Jan-1999
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/689,489
;             FILING DATE: August 12, 1996
;             APPLICATION NUMBER: US 08/231,730
;             FILING DATE: April 20, 1994
;             APPLICATION NUMBER: US 08/225,476
;             FILING DATE: April 8, 1994
;             APPLICATION NUMBER: US 08/039,620
;             FILING DATE: June 4, 1993
;             APPLICATION NUMBER: 08/148,889
;             FILING DATE: No. 6191110ember 8, 1993
;             APPLICATION NUMBER: 08/148,491
;             FILING DATE: No. 6191110ember, 8, 1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Mark J. Bowditch
;             REGISTRATION NUMBER: 40,315
;             REFERENCE/DOCKET NUMBER: 2093-142
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-783-6040
;             TELEFAX: 202-783-6031
;   INFORMATION FOR SEQ ID NO: 42:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 23 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        HYPOTHETICAL: No
;        FRAGMENT TYPE: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-232-802A-42

  Query Match             59.1%;  Score 39;  DB 4;  Length 23;
  Best Local Similarity   53.3%;  Pred. No. 11;
  Matches    8;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |:|| ||:| :
Db          1 FAIAIKAIKKAIKKI 15


RESULT 38
US-09-482-611B-47
; Sequence 47, Application US/09482611B
; Patent No. 6448391
; GENERAL INFORMATION:
;  APPLICANT: Garbarino, Joan
;  APPLICANT:  Belknap, William
;  TITLE OF INVENTION: Ubiquitin Lytic Peptide Fusion Protein Expression
;  TITLE OF INVENTION: Therefrom, and Methods of Making and Using
;  FILE REFERENCE: 2093-149
;  CURRENT APPLICATION NUMBER: US/09/482,611B
;  CURRENT FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: US 08/801,028
;  PRIOR FILING DATE: 1997-02-19
;  PRIOR APPLICATION NUMBER: US 60/039,472
;  PRIOR FILING DATE: 1994-07-22
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
;  LENGTH: 23
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Lytic Peptide
US-09-482-611B-47

  Query Match             59.1%;  Score 39;  DB 4;  Length 23;
  Best Local Similarity   53.3%;  Pred. No. 11;
  Matches    8;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |:|| ||:| :
Db          1 FAIAIKAIKKAIKKI 15


RESULT 39
PCT-US95-04718-42
; Sequence 42, Application PC/TUS9504718
;  GENERAL INFORMATION:
;    APPLICANT:  DEMETER BIOTECHNOLOGIES, LTD.
;    TITLE OF INVENTION:  METHOD OF ENHANCING WOUND HEALING BY STIMULATING FIBRO-B
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FRAN S. WASSERMAN
;      ADDRESSEE:  INTELLECTUAL PROPERTY/TECHN LAW
;      STREET:  200 PARK DRIVE, SUITE 210
;      STREET:  P.O. BOX 14329
;      CITY:  RESEARCH TRIANGLE PARK
;      STATE:  NORTH CAROLINA
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.4 MB STORAGE
;      COMPUTER:  APPLE MACINTOSH
;      OPERATING SYSTEM:  MACINTOSH
;      SOFTWARE:  M.S. WORD 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04718
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/231,730
;      FILING DATE:  20-04-94
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WASSERMAN, FRAN S.
;      REGISTRATION NUMBER:  34273
;      REFERENCE/DOCKET NUMBER:  4013-107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919)990-9531
;      TELEFAX:  (919)990-9532
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23
;      TYPE:  AMINO ACID
;      TOPOLOGY:  LINEAR
```

```
;     MOLECULE TYPE:
;       DESCRIPTION:  PEPTIDE
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  COMPLETE PEPTIDE
;     ORIGINAL SOURCE:  SYNTHETIC
;     IMMEDIATE SOURCE:  SYNTHETIC
;     PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
PCT-US95-04718-42

  Query Match             59.1%;  Score 39;  DB 5;  Length 23;
  Best Local Similarity   53.3%;  Pred. No. 11;
  Matches    8;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |:||: ||:| :
Db          1 FAIAIKAIKKAIKKI 15


RESULT 40
PCT-US95-09338-47
; Sequence 47, Application PC/TUS9509338
;  GENERAL INFORMATION:
;     APPLICANT:
;     TITLE OF INVENTION:  UBIQUITIN-LYTIC PEPTIDE FUSION GENE
;     TITLE OF INVENTION:  CONSTRUCTS, PROTEIN PRODUCTS DERIVING THEREFROM, AND
;     TITLE OF INVENTION:  METHODS OF MAKING AND USING THE SAME
;     NUMBER OF SEQUENCES:  98
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WORDPERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/09338
;       FILING DATE:  21-JUL-1994
;     PRIOR APPLICATION DATA:  08/279,472
;       APPLICATION NUMBER:  08/279,472
;       FILING DATE:  22-JUL-1994
;   INFORMATION FOR SEQ ID NO:  47:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:
;       DESCRIPTION:  PEPTIDE
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  COMPLETE PEPTIDE
;     ORIGINAL SOURCE:  SYNTHETIC
;     IMMEDIATE SOURCE:  SYNTHETIC
;     PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
PCT-US95-09338-47

  Query Match             59.1%;  Score 39;  DB 5;  Length 23;
  Best Local Similarity   53.3%;  Pred. No. 11;
  Matches    8;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |:||: ||:| :
Db          1 FAIAIKAIKKAIKKI 15


RESULT 41
PCT-US95-09339-47
; Sequence 47, Application PC/TUS9509339
;  GENERAL INFORMATION:
;     APPLICANT:
;     APPLICANT:
;     TITLE OF INVENTION:  UBIQUITIN-LYTIC PEPTIDE FUSION GENE
;     TITLE OF INVENTION:  CONSTRUCTS, PROTEIN PRODUCTS DERIVING THEREFROM, AND
;     TITLE OF INVENTION:  METHODS OF MAKING AND USING THE SAME
;     NUMBER OF SEQUENCES:  98
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WORDPERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/09339
;       FILING DATE:  21-JUL-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/279,472
;       FILING DATE:  22-JUL-1994
;   INFORMATION FOR SEQ ID NO:  47:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23
;       TYPE:  AMINO ACID
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:
;       DESCRIPTION:  PEPTIDE
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  COMPLETE PEPTIDE
;     ORIGINAL SOURCE:  SYNTHETIC
;     IMMEDIATE SOURCE:  SYNTHETIC
;     PUBLICATION INFORMATION:  NOT PREVIOUSLY PUBLISHED
PCT-US95-09339-47

  Query Match             59.1%;  Score 39;  DB 5;  Length 23;
  Best Local Similarity   53.3%;  Pred. No. 11;
  Matches    8;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |:||: ||:| :
Db          1 FAIAIKAIKKAIKKI 15


RESULT 42
US-08-232-453A-31
; Sequence 31, Application US/08232453A
; Patent No. 5596058
;  GENERAL INFORMATION:
;     APPLICANT:  HIGASHIJIMA, TSUTOMU
;     APPLICANT:  ROSS, ELLIOTT M.
;     TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;     TITLE OF INVENTION:  MODULATING G PROTEIN ACTION
;     NUMBER OF SEQUENCES:  71
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  ARNOLD, WHITE & DURKEE
;       STREET:  P.O.BOX 4433
;       CITY:  HOUSTON
;       STATE:  TX
;       COUNTRY:  USA
;       ZIP:  77210
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  FLOPPY DISK
;       COMPUTER:  IBM PC COMPATIBLE
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WORDPERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/232,453A
;       FILING DATE:  APRIL 22, 1994
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/248,819
;       FILING DATE:  AUGUST 21, 1991
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  PARKER, DAVID L.
;       REGISTRATION NUMBER:  32,165
;       REFERENCE/DOCKET NUMBER:  [illegible]/TAB
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (512) 418-3000
;       TELEFAX:  (512) 474-7577
;   INFORMATION FOR SEQ ID NO:  31:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  14 amino acids
;       TYPE:  amino acid
```

```
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-232-458A-41

  Query Match             57.6%;  Score 38;  DB 1;  Length 14;
  Best Local Similarity   90.0%;  Pred. No. 9.7;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 KALKALLKAL 12
              :|||| |||
Db          4 KALKALAKAL 13


RESULT 43
US-08-944-133-29
; Sequence 29, Application US/08944133
; Patent No. 5789542
;  GENERAL INFORMATION:
;    APPLICANT:  McLaughlin, Mark L.
;    APPLICANT:  Becker, Calvin L.
;    TITLE OF INVENTION:  Amphipathic Peptides
;    NUMBER OF SEQUENCES:  54
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  John H. Runnels
;      STREET:  P. O. Box 2471
;      CITY:  Baton Rouge
;      STATE:  LA
;      COUNTRY:  USA
;      ZIP:  70821-2471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/944,133
;      FILING DATE:  06-OCT-1997
;      CLASSIFICATION:  5930
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/789,077
;      FILING DATE:  03-FEB-1997
;      APPLICATION NUMBER:  US/08/683,075
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/232,525
;      FILING DATE:  22-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Runnels, John H.
;      REGISTRATION NUMBER:  33451
;      REFERENCE/DOCKET NUMBER:  Atty File No. 5789542 9401
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  504-387-3221
;      TELEFAX:  504-346-8049
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-944-133-29

  Query Match             57.6%;  Score 38;  DB 1;  Length 14;
  Best Local Similarity   81.8%;  Pred. No. 9.7;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 KALKALLKALK 13
              |||| ||||
Db          1 KALEKALEALK 11


RESULT 44
US-07-908-455A-7
; Sequence 7, Application US/07908455A
; Patent No. 5459237
;  GENERAL INFORMATION:
;    APPLICANT:  Berkowitz, Barry A.
;    APPLICANT:  Kari, U. Prasad
;    APPLICANT:  Maloy, W. Lee
;    TITLE OF INVENTION:  New Synthetic Peptide Sarcolectin Analogs
;    TITLE OF INVENTION:  Uses Therefor
;    NUMBER OF SEQUENCES:  89
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cahill, Byrne, Bain, Gilfillan
;      ADDRESSEE:  Cocchi & Stewart
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC DOS
;      SOFTWARE:  DW4.V2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/908,455A
;      FILING DATE:  19920702
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/680,115
;      FILING DATE:  1 APR 1991
;      APPLICATION NUMBER:  US 07/476,29
;      FILING DATE:  08 FEB 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldstein, Elliot M.
;      REGISTRATION NUMBER:  24,529
;      REFERENCE/DOCKET NUMBER:  421.5-122
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 994 1700
;      TELEFAX:  201 994 1744
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      OTHER INFORMATION:  amide terminated
US-07-908-455A-7

  Query Match             57.6%;  Score 38;  DB 1;  Length 21;
  Best Local Similarity   76.9%;  Pred. No. 14;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 KALKALLKALKAL 15
              | |||| | ||||
Db          5 KILKALAKILKAL 17


RESULT 45
US-08-434-120-33
; Sequence 33, Application US/08434120
; Patent No. 5654274
;  GENERAL INFORMATION:
;    APPLICANT:  Baker, Margaret A.
;    APPLICANT:  Jacobs, Leonard S.
;    APPLICANT:  Maloy, W. Lee
;    TITLE OF INVENTION:  Treatment of Dysmenorrhea
;    TITLE OF INVENTION:  Malignancies with
;    TITLE OF INVENTION:  Biologically Active Peptides
;    NUMBER OF SEQUENCES:  117
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cahill, Byrne, Bain, Gilfillan
;      ADDRESSEE:  Cocchi & Stewart
;      STREET:  6 Becker Farm Road
```

```
;       CITY:  Roseland
;       STATE:  New Jersey
;       COUNTRY:  USA
;       ZIP:  07068
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5 inch diskette
;       COMPUTER:  IBM PS/2
;       OPERATING SYSTEM:  PC-DOS
;       SOFTWARE:  DW4.V2
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/434,120
;       FILING DATE:
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/297,950
;       FILING DATE:
;       APPLICATION NUMBER:  US/08/226,108
;       FILING DATE:
;       APPLICATION NUMBER:  US/07/937,462
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Olstein, Elliot M.
;       REGISTRATION NUMBER:  24,025
;       REFERENCE/DOCKET NUMBER:  421250-194
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-994-1700
;       TELEFAX:  201-994-1744
;   INFORMATION FOR SEQ ID NO:  33:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  21 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-434-120-33

  Query Match             57.6%;  Score 38;  DB 1;  Length 21;
  Best Local Similarity   76.9%;  Pred. No. 14;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 KALKALLKALKAL 15
              | |||| | ||||
Db          1 KLLKALGKLLKAL 13


Search completed: August 21, 2003, 09:22:34
Job time : 29 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 21, 2003, 08:06:46 ; Search time 82 Seconds
(without alignments)
29.035 Million cell updates/sec

Title: US-09-820-053A-43
Perfect score: 66
Sequence: 1 FAKALEALLEALFAL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726572 residues

Total number of hits satisfying chosen parameters: 434095

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
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2: /cgn2_6/ptodata/1/pubpaa/A_Geneseq_19Jun03.pep:* combl/AA1987.DAT:*
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24: /cgn2_6/ptodata/1/pubpaa/A_Geneseq_19Jun03.pep:* combl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	66	100.0	15	24	ABR00801	Bioactive synthetic
2	63	90.9	15	24	ABR00910	Bioactive synthetic
3	51	77.3	21	15	AAR58967	Cancer treating, a
4	51	77.3	21	14	AAR45053	Basic (positively
5	51	77.3	21	14	AAR36812	Amphiphilic ion ch
6	51	77.3	21	14	AAR31083	C terminal substd.
7	51	77.3	21	14	AAR35301	Amphiphilic peptid
8	51	77.3	21	14	AAR39015	Biologically activ
9	51	77.3	21	15	AAR55967	Ion channel formin
10	51	77.3	21	15	AAR50489	Amphiphilic peptid
11	51	77.3	21	15	AAR[illegible]	Amphiphilic peptid
12	51	77.3	21	15	AAR[illegible]	[illegible]
13	51	77.3	21	15	AAR[illegible]	(KAESRAL)-peptide
14	51	77.3	21	15	AAR88484	[illegible]
15	51	77.3	21	20	AAY10[illegible]	Peptide toxin [illegible]
16	51	77.3	21	24	AAE22[illegible]	Bi-[illegible]
17	50	75.8	14	19	AAW02[illegible]	Minimalist [illegible]
18	50	75.8	14	19	AAW02[illegible]	Minimalist [illegible]
19	50	75.8	21	19	AAW02[illegible]	Minimalist [illegible]
20	50	75.8	21	19	AAW02[illegible]	Minimalist [illegible]
21	50	75.8	21	19	AAW02[illegible]	Minimalist [illegible]
22	48	72.7	23	11	AAR[illegible]	[illegible]
23	48	72.7	23	15	AAR91[illegible]	[illegible]
24	48	72.7	23	16	AAR77[illegible]	Synthetic [illegible]
25	48	72.7	23	17	AAR02[illegible]	[illegible]
26	48	72.7	23	17	AAR89[illegible]	Synthetic [illegible]
27	48	72.7	23	19	AAW76[illegible]	Bet hexafe[illegible]
28	48	72.7	23	19	AAW99[illegible]	Synthetic [illegible]
29	48	72.7	23	20	AAY10[illegible]	Actin-bind sequence
30	48	72.7	23	20	AAW84[illegible]	[illegible]
31	48	72.7	23	24	ABR[illegible]	[illegible]
32	48	72.7	23	24	ABR[illegible]	[illegible]
33	43	65.2	18	17	AAW[illegible]	Actin-bind [illegible]
34	43	65.2	23	23	AAM4[illegible]	[illegible]
35	43	65.2	23	24	ABR00[illegible]	[illegible]
36	43	65.2	23	24	ABR00[illegible]	[illegible]
37	42	63.6	19	24	ABR0[illegible]	[illegible]
38	42	63.6	19	24	ABR00[illegible]	Bi-active [illegible]
39	42	63.6	20	24	ABR008[illegible]	Bi-active [illegible]
40	42	63.6	23	24	ABR00[illegible]	Bi-active [illegible]
41	42	[illegible]	23	23	ABR00[illegible]	[illegible]
42	42	[illegible]	23	23	ABR00[illegible]	Bi-active [illegible]
43	42	[illegible]	23	23	Abr00[illegible]	[illegible]
44	42	[illegible]	23	23	[illegible]	[illegible]
45	42	[illegible]	23	23	[illegible]	[illegible]

ALIGNMENTS

RESULT 1
ABR00801
ID ABR00801 standard; peptide; [illegible] AA.
XX
AC ABR00801;
XX
DT [illegible] (first entry)
XX
DE Bioactive synthetic peptide [illegible].
XX
KW Antibacterial; Insecticide; cytostatic; veterinary; cancer; cystic fibrosis;
KW [illegible] bioactive; bioactive; [illegible]
KW bioactive.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 15
FT /note "C terminal amide"
XX
PN WO200279408-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009534.
XX
PR 28-MAR-2001; 2001US-279505P.
PR 28-MAR-2001; 2001US-08209[illegible].
XX
PA (HELI) HELIX BIOMEDIX INC.
XX
PI Owen DR;

XX
DR WPI; 2003-221247/21.
XX
PT New isolated peptide for treating cancer, cystic fibrosis, wounds or
PT acne, inhibiting growth of microbial cells, or promoting proliferation
PT of cells, comprises phenylalanine, leucine, alanine or lysine residues
PT
XX
PS Claim 7; Page 6; 133pp; English.
XX
CC The invention relates to a novel isolated peptide which is 5-23 amino
CC acids in length, and comprising phenylalanine, leucine, alanine or lysine
CC residues, or contains at least 50 % of the residues. The peptides of the
CC invention have antibacterial, fungicide, cytostatic, and vulnerary
CC activity. The peptides are useful in treating cancer, cystic fibrosis or
CC acne, inhibiting the growth of microbial cells, promoting the
CC stimulation and/or proliferation of human fibroblasts and lymphocytes,
CC promoting wound healing, and in enhancing the activity of a therapeutic
CC agent. The sequences shown in ABR00759-ABR00923 represent the bioactive
CC peptides of the invention.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 66; DB 24; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAKALKALLKALKAL 15
||||||||||||||||
Db 1 FAKALKALLKALKAL 15

RESULT 2
ABR00910
ID ABR00910 standard; peptide; 15 AA.
XX
AC ABR00910;
XX
DT 03-APR-2003 (first entry)
XX
DE Bioactive synthetic peptide FLAK17CV.
XX
KW Antibacterial; fungicide; cytostatic; vulnerary; cancer; cystic fibrosis;
KW acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
KW bioactive.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 15
FT /note "C-terminal amide"
XX
PN WO200227488-A2.
XX
PD 04-APR-2002.
XX
PF 28-MAR-2002; 2002WO-US09534.
XX
PR 28-MAR-2001; 2001US-279505P.
PR 28-MAR-2001; 2001US-0820053.
XX
PA (HELI-) HELIX BIOMEDIX INC.
XX
PI Owen DR;
XX
DR WPI; 2003-221247/21.
XX
PT New isolated peptide for treating cancer, cystic fibrosis, wounds or
PT acne, inhibiting growth of microbial cells, or promoting proliferation
PT of cells, comprises phenylalanine, leucine, alanine or lysine residues
PT
XX
PS Claim 7; Page 9; 133pp; English.
XX
CC The invention relates to a novel isolated peptide which is 5-23 amino
CC acids in length, and comprising phenylalanine, leucine, alanine or lysine
CC residues, or contains at least 50 % of the residues. The peptides of the
CC invention have antibacterial, fungicide, cytostatic, and vulnerary
CC activity. The peptides are useful in treating cancer, cystic fibrosis or
CC acne, inhibiting the growth of microbial cells, promoting the
CC stimulation and/or proliferation of human fibroblasts and lymphocytes,
CC promoting wound healing, and in enhancing the activity of a therapeutic
CC agent. The sequences shown in ABR00759-ABR00923 represent the bioactive
CC peptides of the invention.
XX
SQ Sequence 15 AA;

Query Match 90.9%; Score 60; DB 24; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AKALKALLKALKAL 15
||||||||||||||
Db 2 AKALKALLKALKAL 15

RESULT 3
AAR58967
ID AAR58967 standard; peptide; 20 AA.
XX
AC AAR58967;
XX
DT 25-MAR-2003 (updated)
DT 20-APR-1995 (first entry)
XX
DE Cancer treating, amphiphilic ion channel forming peptide
XX
KW Amphiphilic ion-channel forming peptide; cancer treatment;
KW protease inhibitors.
XX
OS Synthetic.
XX
PN WO9419369-A1.
XX
PD 01-SEP-1994.
XX
PF 22-FEB-1994; 94WO-US02123.
XX
PR 26-FEB-1993; 93US-0023607.
XX
PA (MAGA) MAGAININ PHARM INC.
XX
PI Berlyn M, Jacob LS, Maloy WL;
XX
DR WPI; 1994-294258/36.
XX
PT Treating cancerous growths - by administering ion channel forming
PT peptide(s) and protease inhibitors.
XX
PS Claim 27; Page 67; 124pp; English.
XX
CC AAR58962 to AAR58967 and AAR58969 to AAR58971 are ion channel forming
CC ion channel forming peptides conforming to the same general
CC sequence. Used in combination with one or more protease
CC inhibitors and other amphiphilic ion channel forming peptides
CC or proteins; they are effective in the treatment of cancerous
CC growths. In particular during surgery and radiation therapy they
CC they may be useful in inhibiting, preventing metastasis of
CC potential "loose" malignant cells capable of spreading to other
CC sites.
CC (Updated on 25 MAR 2003 to correct IN field.)
XX
SQ Sequence 20 AA;

Query Match 77.3%; Score 51; DB 24; Length 20;
Best Local Similarity 85.7%; Pred. No. 0.24;

```
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALEALGKALKAL 15
              :|||||| ||||||
Db          4 SKALKALSKALKAL 17


RESULT 4
AAR45053
ID   AAR45053 standard; peptide; 21 AA.
XX
AC   AAR45053;
XX
DT   25-MAR-2003  (updated)
DT   28-JUN-1994  (first entry)
XX
DE   Basic (positively charged) polypeptide for N terminal
DE   lipophilic substitution.
XX
KW   ion channel; magainin; PGLa; XPF; CPF; cecropin; sarcotoxin;
KW   amphiphilic; hydrophobic; hydrophilic; lipophilic; growth;
KW   inhibition; target cell; virus; virally-infected cell;
KW   antimicrobial; antiviral; antitumour; antiparasitic;
KW   spermicide; wound healing; burn; infection.
XX
OS   Synthetic.
XX
PN   WO9324138-A1.
XX
PD   09-DEC-1993.
XX
PF   27-MAY-1993;   93WO-US05192.
XX
PR   01-JUN-1992;   92US-0891201.
XX
PA   (MAGA ) MAGAININ PHARM INC.
XX
PI   Kari U;
XX
DR   WPI; 1993-405419/50.
XX
PT   Peptide(s) or proteins with an N-terminal lipophilic substit. -
PT   used for inhibiting growth of target cell, virus or
PT   virally-infected cell
XX
PS   Disclosure; Page 75-88; 113pp; English.
XX
CC   A novel compsn. for inhibiting growth of a target cell, virus or
CC   virally-infected cell comprises a peptide of formula T-N(W)-X  (I).
CC   X is a biologically active amphiphilic ion channel-forming peptide
CC   or protein; pref. a magainin peptide, a PGLa peptide, a XPF
CC   peptide, a CPF peptide, a cecropin or a sarcotoxin.
CC   N is the nitrogen of the N-terminal amino group.
CC   T is a lipophilic moiety; pref. R-CO, where R is a 2-16C
CC   hydrocarbon (alkyl or aromatic or alkylaromatic).
CC   T is pref. an octanoyl group.
CC   W is T or hydrogen.
CC   The peptides given in AAR45041-89 are examples of X.
CC   The N terminal substd. peptides and proteins have increased
CC   biological activity as compared with unsubstd. peptides or proteins
CC   or peptides substd. at the N terminal with an acetyl gp.
CC   They can be used as antimicrobial agents, antiviral agents,
CC   antitumour agents, antiparasitic agents or spermicides and
CC   can also exhibit other biological functions. They can also be
CC   used in promoting or stimulating wound healing, for the treatment
CC   of external burns and for treating and/or preventing skin and burn
CC   infections or eye infections.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence   21 AA;

  Query Match             77.3%;  Score 51;  DB 14;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.25;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALEALGKALKAL 15
              :|||||| ||||||
Db          4 SKALKALSKALKAL 17


RESULT 5
AAR36312
ID   AAR36312 standard; peptide; 21 AA.
XX
AC   AAR36312;
XX
DT   25-MAR-2003  (updated)
DT   24-AUG-1993  (first entry)
XX
DE   Amphiphilic ion channel forming peptide.
XX
KW   Growth; inhibition; antibiotic; tumour; parasitic; XPF; PGLa; CPF;
KW   tetracycline; pseudomonic acid; neomycin.
XX
OS   Synthetic.
XX
PN   WO9307892-A1.
XX
PD   29-APR-1993.
XX
PF   16-OCT-1992;   92WO-US08823.
XX
PR   16-OCT-1991;   91US-0778771.
XX
PA   (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
XX
PI   Berkowitz B;  Zasloff M;
XX
DR   WPI; 1993-154184/18.
XX
PT   Inhibiting growth of bacteria  by co-administration of
PT   antibiotic and ion channel-forming peptide, e.g. magainin
XX
PS   Disclosure; Page 26; 125pp; English.
XX
CC   The sequence is that of a basic polypeptide of at least 8 hydrophobic
CC   amino acids and at least 8 hydrophilic amino acids. The peptide is
CC   amphiphilic, positively charged and ion channel-forming and may
CC   be used in a compsn. with an antibiotic which is not an ion channel
CC   forming peptide, to inhibit the growth of target cells. The peptide
CC   is pref. a magainin peptide, XPF, PGLa or CPF peptide. The peptide
CC   and antibiotic potentiate each other, i.e. interaction of the
CC   peptide with the membranes of bacterial cells facilitates
CC   penetration of the cells by the antibiotic. The compsn. thus
CC   requires less antibiotic and may have extended use as the
CC   antibiotic alone. Apart from therapeutic use the peptides can be
CC   used as preservatives or sterilants.
CC   See also AAR36281-380.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence   21 AA;

  Query Match             77.3%;  Score 51;  DB 14;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.25;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALEALGKALKAL 15
              :|||||| ||||||
Db          4 SKALKALSKALKAL 17


RESULT 6
AAR31083
ID   AAR31083 standard; peptide; 21 AA.
XX
AC   AAR31083;
```

```
XX
DT   25-MAR-2003  (updated)
DT   10-MAY-1994  (first entry)
XX
DE   C-terminal substd. amphiphilic peptide #32.
XX
KW   ion-channel forming; ionophore; antibiotic; anti-tumour; anti virus;
KW   wound healing.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1..7
FT                   /label= repeat_unit
FT   Modified-site   21
FT                   /note= "Leu-(C O) T,
FT                          T  O R, NH NH2, NH OH or NR'R",
FT                          R  opt.substd. 1-10C aliphatic, aromatic or
FT                             aralkyl qp.;
FT                          R', R"- H or from one of qps. i and ii;
FT                          qp.i  1-10C hydroxy-substd. aliphatic,
FT                                aromatic or aralkyl qp.;
FT                          qp.ii  amino-substd. aliphatic, aromatic,
FT                                 aralkyl or alkylaromatic qp. and
FT                          at least one of R' and R"  qp.i or qp.ii"
XX
PN   WO9222317-A1.
XX
PD   23-DEC-1992.
XX
PF   01-JUN-1992;   92WO-US004603.
XX
PR   12-JUN-1991;   91US-0713716.
XX
PA   (MAGA-) MAGAININ PHARM INC.
XX
PI   Kari OP,  Maloy WL;
XX
DR   WPI; 1993-017904/02.
XX
PT   New C-terminal-substd. amphiphilic peptide(s) - for treating
PT   bacterial, viral or fungal infections and tumours, also useful as
PT   spermicide
XX
PS   Claim 10; Page 76; 124pp; English.
XX
CC   This peptide is a preferred example of a highly generic amphiphilic
CC   peptide with a C-terminal modification which increases the peptide's
CC   biological activity c.f. the unmodified peptide. The preferred
CC   C-terminal modification is -(CO)-NHCH2CH2OH or -(CO)-NHCH2CH2NH2.
CC   Such substd. peptides may be used for inhibiting the growth of a
CC   target cell, virus or virally infected cell in a host. The peptides
CC   have a broad range of potent antibiotic activity, e.g. against gram-
CC   negative and gram positive bacteria, fungi, protozoa and parasites.
CC   The peptides can also be used to promote wound healing and treatment
CC   of burns. Other preferred amphiphilic peptides include magainins and
CC   their analogues, PGLa, XPF, CPF, a cecropin and a sarcotoxin.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence   21 AA;

  Query Match             77.3%;  Score 51;  DB 14;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.25;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              :|||||| ||||||
Db          4 SKALKALSKALKAL 17


RESULT 7
AAR35401
ID   AAR35401 standard; peptide; 21 AA.
XX
AC   AAR35401;
XX
DT   25-MAR-2003  (updated)
DT   07-JUN-1993  (first entry)
XX
DE   Amphiphilic peptide #32 used to treat oral infections.
XX
KW   Adverse oral conditions; amphipathic; anti-bacterial; anti-viral;
KW   anti-fungal; dental plaque; dental caries; periodontal disease;
KW   gingivitis; ionophore; ion channel forming.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1..7
FT                   /note= "repeat unit"
XX
PN   WO9301723-A1.
XX
PD   04-FEB-1993.
XX
PF   09-JUL-1992;   92WO-US005757.
XX
PR   25-JUL-1991;   91US-0735070.
XX
PA   (MAGA-) MAGAININ PHARM INC.
XX
PI   Berkowitz B,  Jacob L;
XX
DR   WPI; 1993-058434/07.
XX
PT   Peptide(s) for prophylaxis and treatment of oral disorders - used
PT   for periodontal disease, plaque, dental caries, gingivitis etc.
XX
PS   Claim 2; Page 92; 143pp; English.
XX
CC   This is a specific example of a highly generic family of peptides
CC   preferred amphiphilic peptides for use in prophylaxis & treatment
CC   adverse oral conditions. The peptide is an antagonist (i.e. an anti-
CC   channel forming peptide) which has anti bacterial, anti viral, anti
CC   fungal activity, etc. making it suitable for use in the topical
CC   to treat or prevent periodontal disease, plaque, dental caries,
CC   halitosis and gingivitis. The anti bacterial acts & peptides are
CC   useful against bacteria associated with dental caries and periodontal
CC   the peptides can stimulate the healing of wounds in the oral cavity.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence   21 AA;

  Query Match             77.3%;  Score 51;  DB 14;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.25;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              :|||||| ||||||
Db          4 SKALKALSKALKAL 17


RESULT 8
AAR39015
ID   AAR39015 standard; peptide; 21 AA.
XX
AC   AAR39015;
XX
DT   25-MAR-2003  (updated)
DT   08-NOV-1993  (first entry)
XX
DE   Biologically active amphiphilic peptide.
XX
KW   Synergistic antimicrobial composition; combin...  ...ial agent;
KW   combination; preservative; sterilant; animal; p...  ...;
KW   control; treatment; prevention; external burns, ...  ...
```

```
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   21
FT                   /note= "amide terminated"
XX
PN   WO9311783-A1.
XX
PD   24-JUN-1993.
XX
PF   03-DEC-1992;    92WO-US10427.
XX
PR   09-DEC-1991;    91US-0803629.
XX
PA   (MAGA ) MAGAININ PHARM INC.
XX
PI   Berkowitz B;
XX
DR   WPI; 1993-214816/26.
XX
PT   Synergistic antimicrobial compsn. for treating or preventing
PT   infection of burns - contg. amphiphilic peptide or protein e.g.
PT   magainin peptide and chelating agent
XX
PS   Example; Page 24; 122pp; English.
XX
CC   The sequence is that of a biologically active amphiphilic peptide
CC   which is used in a synergistic antimicrobial compsn. with a
CC   chelating agent. The chelating agent potentiates the activity of the
CC   peptide by binding inhibitory Ca/Mg ions and may also increase
CC   permeability of the target cells to the peptide. The compsn. is
CC   active against a wide range of microorganisms (esp. bacteria) and
CC   can be used as a preservative or sterilant, or to control infections
CC   in animals or plants. Particular applications are to treat/prevent
CC   infections of external burns and treatment of eye infections e.g.
CC   where the pathogen is Pseudomonas aeruginosa, Staphylococcus aureus,
CC   Streptococcus or Neisseria gonorrhoeae.
CC   (Updated on 25-MAR 2003 to correct PN field.)
XX
SQ   Sequence   21 AA;

  Query Match             77.3%;  Score 51;  DB 14;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.25;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              :|||||| |||||
Db          4 SKALKALSKALKAL 17


RESULT 9
AAR55907
ID   AAR55907 standard; peptide; 21 AA.
XX
AC   AAR55907;
XX
DT   25-MAR-2003  (updated)
DT   16-DEC-1994  (first entry)
XX
DE   Ion channel forming peptide.
XX
KW   Ion channel forming peptide; tumour; skin disease; malignancy;
KW   melanoma; carcinoma; basal cell; squamous cell; magainin; PGLa;
KW   CPF peptides; cecropins; sarcotoxin; melittin; apidaecin; defensins;
KW   major basic protein; bacteria-permeability increasing protein;
KW   perforin.
XX
OS   Synthetic.
XX
PN   WO9412206-A1.
XX
PD   09-JUN-1994.
XX
PF   03-DEC-1993;    93WO-US11885.
XX
PR   03-DEC-1992;    92US-0984057.
XX
PA   (MAGA ) MAGAININ PHARM INC.
XX
PI   Jacob LS,  Maloy WL;
XX
DR   WPI; 1994-199965/24.
XX
PT   Treating skin cancer with ion channel forming peptide(s) - e.g.
PT   magainins, melittin etc., specifically for treating melanoma
XX
PS   Disclosure; Page 84; 139pp; English.
XX
CC   The peptide is used to treat dermatological malignancies. It
CC   may be used to treat especially melanoma but also basal cell and
CC   squamous cell carcinomas. It can be used together with an ion which
CC   also inhibits/prevents growth of the target cell. Peptides used for
CC   such therapy include magainin, PGLa or CPF peptides; cecropins,
CC   sarcotoxins, melittin, apidaecins, defensins and major basic protein.
CC   eosinophils; bacteria-permeability increasing protein; etc. active
CC   See also AAQ55876-Q55897.
CC   (Updated on 25 MAR 2003 to correct PN field.)
XX
SQ   Sequence   21 AA;

  Query Match             77.3%;  Score 51;  DB 15;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.25;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              :|||||| |||||
Db          4 SKALKALSKALKAL 17


RESULT 10
AAR60483
ID   AAR60483 standard; peptide; 21 AA.
XX
AC   AAR60483;
XX
DT   25-MAR-2003  (updated)
DT   18-OCT-1994  (first entry)
XX
DE   Amphiphillic peptide #32.
XX
KW   Amphiphilic; ion forming; gynaecological malignancy; melanin; PGLa;
KW   XPF; CPF; cecropin; sarcotoxin; melittin; apidaecin; defensin;
KW   major basic protein; eosinophils; porcine; cervical; cancer;
KW   bacterial permeability increasing protein; ovarian; stage 2.
XX
OS   Synthetic.
XX
PN   WO9404573-A1.
XX
PD   17-MAR-1994.
XX
PF   16-AUG-1993;    93WO-US07798.
XX
PR   31-AUG-1992;    92US-0937462.
XX
PA   (MAGA ) MAGAININ PHARM INC.
XX
PI   Baker MA,  Jacob LS,  Maloy WL;
XX
DR   WPI; 1994-100857/12.
XX
PT   Treating gynaecological tumours with amphiphilic peptide(s)
PT   which form ion channels, e.g. magainin or PGLa peptide(s)
PT   particularly for treating ovarian, uterine or cervical cancers
XX
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PS   Disclosure; Page 79; 130pp; English.
XX
CC   The sequences given in AAR50452-568 represent amphiphilic, ion forming
CC   peptides which may be used to treat gynaecological malignancy.
CC   These peptides are based on magainin, PGLa, XPF or CPF, a cecropin, a
CC   sarcotoxin, melittin, an apidaecin, a defensin, major basic protein of
CC   eosinophils or a bacterial permeability increasing protein.  These
CC   peptides are esp. used to treat ovarian, esp. stage IC, uterine or
CC   cervical cancers.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence   21 AA;

  Query Match             77.3%;  Score 51;  DB 15;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.25;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           2 AKALKALLKALKAL 15
               :|||||| ||||||
Db           4 SKALKALSKALKAL 17


RESULT 11
AAR50367
ID   AAR50367 standard; peptide; 21 AA.
XX
AC   AAR50367;
XX
DT   25-MAR-2003  (updated)
DT   17-OCT-1994  (first entry)
XX
DE   Amphiphilic peptide #42.
XX
KW   Amphiphilic peptide; aprotic organic solvent; alcohol; antitumour;
KW   antibiotic; antimicrobial, antifungal, antiparasitic; anticancer;
KW   antiviral, human, animal; plant; ion-channel; forming peptide.
XX
OS   Synthetic.
XX
PN   WO9405308-A1.
XX
PD   17-MAR-1994.
XX
PF   13-AUG-1993;   93WO-US07694.
XX
PR   28-AUG-1992;   92US-0936504.
XX
PA   (MAGA ) MAGAININ PHARM INC.
XX
PI   Williams JI;
XX
DR   WPI; 1994-100846/12.
XX
PT   Purifying amphiphilic protein or peptide by solvent extn. -
PT   partic. for recombinant, ion-channel forming peptide(s) such as
PT   magainins, avoids use of chaotropic agents.
XX
PS   Disclosure; Page 84-85; 135pp; English.
XX
CC   The sequences given in AAR50326-451 are amphiphilic peptides which
CC   were isolated by the method of the invention.  A material containing
CC   amphiphilic peptides such as these, was treated with a mixt. of
CC   aprotic organic solvent and alcohol to form a single miscible
CC   solution.  This solution was then treated with a aqueous solution to
CC   form an aqueous phase solution contatining the peptides and an
CC   organic solvent phase, and the peptides were isolated from the
CC   aqueous phase.  The isolated peptides may be useful as antibiotic,
CC   antimicrobial, antifungal, antiparasitic, antitumour, anticancer,
CC   and/or antiviral agents for treatment of humans, animals or plants.
CC   These peptides are esp. ion channel forming peptides which enable
CC   biologically active ions to enter cells.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence   21 AA;

  Query Match             77.3%;  Score 51;  DB 15;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.25;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           2 AKALKALLKALKAL 15
               :|||||| ||||||
Db           4 SKALKALSKALKAL 17


RESULT 12
AAR55622
ID   AAR55622 standard; peptide; 21 AA.
XX
AC   AAR55622;
XX
DT   25-MAR-2003  (updated)
DT   16-MAR-1995  (first entry)
XX
DE   Peptide which neutralises bacterial endotoxin.
XX
KW   septic shock; bacterial endotoxin; lipopolysaccharide; LPS;
KW   gram negative bacteria; conjugate moiety; septicaemia; bacteraemia;
KW   longer activity; polyvinylpyrrolidone; dextran; polyethylene
KW   polyvinyl alcohol; ion channel forming; amphiphilic.
XX
OS   Synthetic.
XX
PN   WO9413697-A1.
XX
PD   23-JUN-1994.
XX
PF   09-DEC-1993;   93WO-US11841.
XX
PR   07-DEC-1992;   92US-0987443.
XX
PA   (MAGA ) MAGAININ PHARM INC.
XX
PI   Houdi M;  Kao M;  Williams LI;
XX
DR   WPI; 1994-217804/26.
XX
PT   New conjugates of bioactive amphiphilic peptides, e.g. ion channel
PT   moiety - are useful for treatment of septic shock.
XX
PS   Disclosure; Page 76-77; 141pp; English.
XX
CC   Septic shock is often due to the body's reaction to bacterial
CC   lipopolysaccharide (LPS). The compounds of the invention neutralise
CC   bacterial endotoxins without neutralising essential proteins, e.g.
CC   plasma of patients, eg. heparins. They also have longer activity
CC   activity than unconjugated peptides. In general peptides which are
CC   are ion channel forming peptides. The compounds are of the formula
CC   peptides linked to a conjugate moiety, eg. carbohydrates, e.g.
CC   polyvinylpyrrolidone, polyalkylene glycols and polyvinyl alcohol.
CC   The conjugate moiety may be linked at the C- or N-terminal, or
CC   internally of the peptide.  AAR55601-631 and AAR55632-662 are amino
CC   of these peptide conjugate moiety compounds.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence   21 AA;

  Query Match             77.3%;  Score 51;  DB 15;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.25;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           2 AKALKALLKALKAL 15
               :|||||| ||||||
Db           4 SKALKALSKALKAL 17


RESULT 13
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AAR90075
ID   AAR90075 standard; peptide; 21 AA.
XX
AC   AAR90075;
XX
DT   03-JUL-1996  (first entry)
XX
DE   (KALSKAL)3 peptide modified by N-terminal lipophilic group.
XX
KW   Ion channel forming peptide; lipophilic; N-terminal modification;
KW   magainin; inhibition; cell growth; viral replication; ionophore;
KW   membrane permeability; antimicrobial; anti-bacterial; antibiotic;
KW   anti-fungal; anti-viral; spermicidal; anti-tumour; anti-parasitic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-terminal amino group is mono- or
FT                    di-substd. by lipophilic moiety, esp.
FT                    octanoyl"
FT   Peptide         1..7
FT                   /label= repeat
FT                   /note= "first of 3 repeats of amphipathic
FT                    heptapeptide motif"
XX
PN   WO9519370-A1.
XX
PD   20-JUL-1995.
XX
PF   18-JAN-1995;    95WO-US00714.
XX
PR   18-JAN-1994;    94US-0184462.
XX
PA   (MAGA-) MAGAININ PHARM INC.
XX
PI   Kari UP,  McLane M,  Williams TJ;
XX
DR   WPI; 1995-263826/34.
XX
PT   Ion channel-forming amphiphilic peptide(s) with N-terminal
PT   lipophilic grps. - useful e.g. as antiviral, antibacterial,
PT   antiparasitic or antitumour agents
XX
PS   Claim 21; Page 78; 139pp; English.
XX
CC   The present peptide is a specific example corresp. to a highly
CC   generic formula for ion channel forming peptides (ionophores)
CC   consisting of 1-5 repeats of an amphipathic heptapeptide motif.
CC   These ionophores are known to have a broad range of potent
CC   antibiotic activity against microorganisms including gram-positive
CC   and gram-negative bacteria, fungi, viruses, protozoa and parasites.
CC   N-terminal modification (pref. mono-substn. by octanoyl) to produce
CC   an ion channel forming peptide having a lipophilic N-terminus
CC   increases the biological activity of the peptides against target cells,
CC   viruses and virally-infected cells, compared to peptides substd. with
CC   an acetyl group at the N-terminus. Compositions comprising the peptides
CC   with lipophilic modifications are claimed for inhibiting growth of a
CC   target cell, virus or virally-infected cell.
XX
SQ   Sequence   21 AA;

  Query Match             77.3%;  Score 51;  DB 16;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.25;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              :|||||| ||||||
Db          4 SKALKALSKALKAL 17


RESULT 14
AAR83846
ID   AAR83846 standard; peptide; 21 AA.
XX
AC   AAR83846;
XX
DT   25-MAR-2003  (updated)
DT   24-MAY-1996  (first entry)
XX
DE   Ion channel forming amphiphilic peptide #6.
XX
KW   Ion-channel; amphiphilic peptide; antimicrobial; antiviral; antibiotic;
KW   antitumour; antiparasitic; antifungal; spermicide; cyst; spore; skin;
KW   trophozoite; infection; wound healing; burn.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 21
FT                   /note= "contains C terminal amide group"
XX
PN   US5459237-A.
XX
PD   17-OCT-1995.
XX
PF   02-JUL-1992;    92US-0908455.
XX
PR   02-JUL-1992;    92US-0908455.
PR   08-FEB-1990;    90US-0476629.
PR   15-APR-1991;    91US-0686115.
XX
PA   (MAGA-) MAGAININ PHARM INC.
XX
PI   Berkowitz B,  Kari UP,  Maloy WL;
XX
DR   WPI; 1995-365836/47.
XX
PT   New ion channel-forming amphiphilic peptide(s)  useful as
PT   antimicrobial, antiviral, antitumour, antiparasitic or antifungal
PT   agents or for wound healing
XX
PS   Disclosure; Column 5; 38pp; English.
XX
CC   The peptides AAR83841-R83908 are examples of novel ion-channel forming
CC   amphiphilic peptides which can be used as antimicrobial, antiviral,
CC   antibiotic, antitumour, antiparasitic, antifungal agents or as
CC   spermicides.  The peptides can be used as preservatives or sterilants
CC   for materials susceptible to microbial or viral infections.  The
CC   peptides can also be used for killing cysts, spores or trophozoites of
CC   infection-causing organisms.  They can also be used to promote wound
CC   healing or to treat or prevent skin and burn infections.  The peptides
CC   can be administered in combination with other biologically active
CC   amphiphilic peptides such as AAR83909-29.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence   21 AA;

  Query Match             77.3%;  Score 51;  DB 16;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 0.25;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              :|||||| ||||||
Db          4 SKALKALSKALKAL 17


RESULT 15
AAY10671
ID   AAY10671 standard; peptide; 21 AA.
XX
AC   AAY10671;
XX
DT   11-MAY-1999  (first entry)
XX
DE   Peptide used to make biologically active peptides.
```

XX
KW Sepsis; septic shock; Pseudomonas aeruginosa; cystic fibrosis;
KW antimicrobial; antiviral; antibacterial; antifungal; antitumour;
KW antiparasitic; spermicide; preservative; sterilant; disinfectant;
KW wound healing; burn; skin infection; eye infection; solid tumour;
KW leukaemia; non-small cell lung cancer; adenocarcinoma; plant infection;
KW periodontal disease; plaque; gingivitis; caries; Streptococcus mutans.
XX
OS Synthetic.
XX
PN WO9901488-A2.
XX
PD 28-JAN-1999.
XX
PF 15-JUL-1998; 98WO-US14610.
XX
PR 15-JUL-1997; 97US-0893006.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Kari UP, McLane M, Williams TJ;
XX
DR WPI; 1999-141859/11.
XX
PT Treating sepsis or septic shock with N-modified ion-channel forming
PT peptide - or its methane sulphonate derivative of reduced toxicity,
PT also generally useful as antimicrobial and antitumour agents
XX
PS Disclosure; Page 154; 202pp; English.
XX
CC AAY10640 796 represent peptides used in the production of biologically
CC active peptides with reduced toxicity. The biologically active peptides
CC are used to treat sepsis or septic shock, and comprise the formula:
CC I N(W) X, where X = biologically active, amphipathic, ion-channel
CC forming peptide or protein; I = lipophilic group; and W = hydrogen or T.
CC The peptides are particularly used to treat infections by Pseudomonas
CC aeruginosa in patients with cystic fibrosis, but more generally as
CC anti-microbial, antiviral, antibacterial, antifungal, antitumour or
CC antiparasitic agents, and also as spermicides, e.g. as preservatives,
CC sterilants, and disinfectants in human and veterinary medicine. They
CC can be used to stimulate wound healing, treat burns and/or skin and
CC burn infections, eye infections, solid tumours or leukaemia
CC (particularly non-small cell lung cancer and adenocarcinoma, including
CC those resistant to other antitumour agents), and also for treatment of
CC infections in plants, and, when formulated in oral hygiene formulations,
CC for treating or preventing periodontal disease, plaque, gingivitis and/or
CC caries (specifically by action on Streptococcus mutans).
XX
SQ Sequence 21 AA;

Query Match 77.3%; Score 51; DB 20; Length 21;
Best Local Similarity 85.7%; Pred. No. 0.25;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AKAIKAEIKALKAL 15
:|||||| ||||||
Db 4 SKALKALSKALKAL 17

RESULT 16
AAE22384
ID AAE22384 standard; peptide; 21 AA.
XX
AC AAE22384;
XX
DT 25-JUL-2002 (first entry)
XX
DE Biologically active peptide #16.
XX
KW Biologically active peptide; toxicity; antimicrobial; anti tumour;
KW methane sulphonate derivative; wound healing; burn; therapy; sepsis;
KW eye infection; cyst; spore; trophozoite; tumour; lung infection;
KW cystic fibrosis; septic shock; bacterial endotoxin; cytostatic;
KW antibacterial; immunosuppressive.
XX
OS Unidentified.
XX
PN US6348445-B1.
XX
PD 19-FEB-2002.
XX
PF 15-JUL-1998; 98US-0115737.
XX
PR 18-JAN-1994; 94US-0184402.
PR 01-JUN-1992; 92US-0891201.
PR 05-JUN-1995; 95US-0465830.
PR 15-JUL-1997; 97US-0893006.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Kari UP, Williams TJ, McLane M;
XX
DR WPI; 2002-[illegible]/08.
XX
PT Reducing toxicity of unsubstituted or N-terminal substituted peptides
PT having antimicrobial and antitumor activity useful in treating
PT infections and tumor, by forming methane [illegible]
PT of peptide
XX
PS Disclosure; Column 17; 78pp; English.
XX
CC The invention relates to biologically active peptides with reduced
CC toxicity and methods of preparing them. The peptides of
CC the invention have improved antimicrobial and [illegible]
CC while exhibiting reduced toxicity. The method [illegible]
CC involves the formation of related methane [illegible]
CC analogues. The method is useful for reducing [illegible]
CC unsubstituted peptide or an N-terminal substituted peptide which is
CC utilised in promoting or stimulating healing of a wound in a [illegible]
CC treatment of external burns, prevention or treatment [illegible]
CC caused by bacteria or fungi, in killing cysts [illegible]
CC of infection causing organisms, and may also be employed in the
CC treatment of tumours, serious lung infections such as those occurring
CC in cystic fibrosis, for treating sepsis, septic shock [illegible]
CC related ailments, and for neutralising bacterial endotoxin. The
CC present sequence is a biologically active peptide [illegible]
XX
SQ Sequence 21 AA;

Query Match 77.3%; Score 51; DB 20; Length 21;
Best Local Similarity 85.7%; Pred. No. 0.25;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AKAIKAEIKALKAL 15
:|||||| ||||||
Db 4 SKALKALSKALKAL 17

RESULT 17
AAW62949
ID AAW62949 standard; peptide; 14 AA.
XX
AC AAW62949;
XX
DT 02-OCT-1998 (first entry)
XX
DE Minimalist lytic peptide.
XX
KW Lytic peptide; channel forming peptide; antibacterial; antiparasitic;
XX
OS Synthetic.
XX
PN US5789542-A.
XX
PD 04-AUG-1998.
XX

```
PF   06-OCT-1997;   97US-0944133.
XX
PR   22-APR-1994;   94US-0232525.
PR   22-JUL-1996;   96US-0681075.
PR   03-FEB-1997;   97US-0789077.
PR   06-OCT-1997;   97US-0944133.
XX
PA   (LOUU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
XX
PI   Becker CL,  McLaughlin ML;
XX
DR   WPI; 1998-446183/38.
XX
PT   Selective lysis of bacteria amongst mammalian cells - using 14-mer
PT   or 21-mer lytic peptides
XX
PS   Claim 7; Column 35; 25pp; English.
XX
CC   AAW62920-67 represent minimalist lytic (channel forming) peptides. The
CC   peptides have antibacterial properties in concentrations not lethal
CC   toward mammalian cells. The peptides are heptads (or heptad multimers)
CC   that comprise four nonpolar amino acid residues and three positively
CC   charged amino acid residues, or five nonpolar amino acid residues and
CC   two positively charged amino acid residues. The nonpolar amino acid
CC   residues and the positively charged amino acid residues are distributed
CC   within the heptad such that when the multimer forms an alpha-helix the
CC   nonpolar amino acid residues will lie on one face of the alpha-helix,
CC   and the positively charged amino acid residues will lie on the opposite
CC   face of the alpha -helix, whereby the multimer is amphipathic.
XX
SQ   Sequence   14 AA;

  Query Match             75.8%;  Score 50;  DB 19;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 0.24;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           3 KALKALLKALKAL 15
               ||||||  ||||||
Db           2 KALKALKKALKAL 14


RESULT 18
AAW62933
ID   AAW62933 standard; peptide; 14 AA.
XX
AC   AAW62933;
XX
DT   02-OCT-1998  (first entry)
XX
DE   Minimalist lytic peptide.
XX
KW   Lytic peptide; channel forming peptide; antibacterial; amphipathic.
XX
OS   Synthetic.
XX
PN   US5789542-A.
XX
PD   04-AUG-1998.
XX
PF   06-OCT-1997;   97US-0944133.
XX
PR   22-APR-1994;   94US-0232525.
PR   22-JUL-1996;   96US-0681075.
PR   03-FEB-1997;   97US-0789077.
PR   06-OCT-1997;   97US-0944133.
XX
PA   (LOUU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
XX
PI   Becker CL,  McLaughlin ML;
XX
DR   WPI; 1998-446183/38.
XX
PT   Selective lysis of bacteria amongst mammalian cells - using 14-mer
PT   or 21-mer lytic peptides
XX
PS   Claim 6; Column 35; 25pp; English.
XX
CC   AAW62920-67 represent minimalist lytic (channel forming) peptides. The
CC   peptides have antibacterial properties in concentrations not lethal
CC   toward mammalian cells. The peptides are heptads (or heptad multimers)
CC   that comprise four nonpolar amino acid residues and three positively
CC   charged amino acid residues, or five nonpolar amino acid residues and
CC   two positively charged amino acid residues. The nonpolar amino acid
CC   residues and the positively charged amino acid residues are distributed
CC   within the heptad such that when the multimer forms an alpha-helix the
CC   nonpolar amino acid residues will lie on one face of the alpha-helix,
CC   and the positively charged amino acid residues will lie on the opposite
CC   face of the alpha -helix, whereby the multimer is amphipathic.
XX
SQ   Sequence   14 AA;

  Query Match             75.8%;  Score 50;  DB 19;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 0.24;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           3 KALKALLKALKAL 15
               ||||||  ||||||
Db           1 KALKALKKALKAL 13


RESULT 19
AAW62946
ID   AAW62946 standard; peptide; 21 AA.
XX
AC   AAW62946;
XX
DT   02-OCT-1998  (first entry)
XX
DE   Minimalist lytic peptide.
XX
KW   Lytic peptide; channel forming peptide; antibacterial; amphipathic.
XX
OS   Synthetic.
XX
PN   US5789542-A.
XX
PD   04-AUG-1998.
XX
PF   06-OCT-1997;   97US-0944133.
XX
PR   22-APR-1994;   94US-0232525.
PR   22-JUL-1996;   96US-0681075.
PR   03-FEB-1997;   97US-0789077.
PR   06-OCT-1997;   97US-0944133.
XX
PA   (LOUU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
XX
PI   Becker CL,  McLaughlin ML;
XX
DR   WPI; 1998-446183/38.
XX
PT   Selective lysis of bacteria amongst mammalian cells - using 14-mer
PT   or 21-mer lytic peptides
XX
PS   Disclosure; Column 6; 25pp; English.
XX
CC   AAW62920-67 represent minimalist lytic (channel forming) peptides. The
CC   peptides have antibacterial properties in concentrations not lethal
CC   toward mammalian cells. The peptides are heptads (or heptad multimers)
CC   that comprise four nonpolar amino acid residues and three positively
CC   charged amino acid residues, or five nonpolar amino acid residues and
CC   two positively charged amino acid residues. The nonpolar amino acid
CC   residues and the positively charged amino acid residues are distributed
CC   within the heptad such that when the multimer forms an alpha-helix the
CC   nonpolar amino acid residues will lie on one face of the alpha-helix,
CC   and the positively charged amino acid residues will lie on the opposite
```

```
CC   face of the alpha  helix, whereby the multimer is amphipathic.
XX
SQ   Sequence   21 AA;

  Query Match             75.8%;  Score 50;  DB 19;  Length 21;
  Best Local Similarity   92.3%;  Pred. No. 0.46;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 KALKALLKALKAL 15
              |||||| ||||||
Db          5 KALKALKKALKAL 17


RESULT 20
AAW62950
ID   AAW62950 standard; peptide; 21 AA.
XX
AC   AAW62950;
XX
DT   02-OCT-1998  (first entry)
XX
DE   Minimalist lytic peptide.
XX
KW   Lytic peptide; channel forming peptide; antibacterial; amphipathic.
XX
OS   Synthetic.
XX
PN   US5789542-A.
XX
PD   04-AUG-1998.
XX
PF   06-OCT-1997;   97US-0944133.
XX
PR   22-APR-1994;   94US-0232525.
PR   22-JUL-1996;   96US-0681075.
PR   03-FEB-1997;   97US-0789077.
PR   06-OCT-1997;   97US-0944133.
XX
PA   (LOUU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
XX
PI   Boecker CL,  McLaughlin ML;
XX
DR   WPI; 1998-446183/38.
XX
PT   Selective lysis of bacteria amongst mammalian cells - using 14-mer
PT   or 21 mer lytic peptides
XX
PS   Disclosure; Column 6; 25pp; English.
XX
CC   AAW62920-67 represent minimalist lytic (channel forming) peptides. The
CC   peptides have antibacterial properties in concentrations not lethal
CC   toward mammalian cells. The peptides are heptads (or heptad multimers)
CC   that comprise four nonpolar amino acid residues and three positively
CC   charged amino acid residues, or five nonpolar amino acid residues and
CC   two positively charged amino acid residues. The nonpolar amino acid
CC   residues and the positively charged amino acid residues are distributed
CC   within the heptad such that when the multimer forms an alpha helix the
CC   nonpolar amino acid residues will lie on one face of the alpha-helix,
CC   and the positively charged amino acid residues will lie on the opposite
CC   face of the alpha  helix, whereby the multimer is amphipathic.
XX
SQ   Sequence   21 AA;

  Query Match             75.8%;  Score 50;  DB 19;  Length 21;
  Best Local Similarity   92.3%;  Pred. No. 0.46;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 KALKALLKALKAL 15
              |||||| ||||||
Db          2 KALKALKKALKAL 14


RESULT 21
```

```
AAW62934
ID   AAW62934 standard; peptide; 21 AA.
XX
AC   AAW62934;
XX
DT   02-OCT-1998  (first entry)
XX
DE   Minimalist lytic peptide.
XX
KW   Lytic peptide; channel forming peptide; antibacterial; amphipathic.
XX
OS   Synthetic.
XX
PN   US5789542-A.
XX
PD   04-AUG-1998.
XX
PF   06-OCT-1997;   97US-0944133.
XX
PR   22-APR-1994;   94US-0232525.
PR   22-JUL-1996;   96US-0681075.
PR   03-FEB-1997;   97US-0789077.
PR   06-OCT-1997;   97US-0944133.
XX
PA   (LOUU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
XX
PI   Boecker CL,  McLaughlin ML;
XX
DR   WPI; 1998-446183/38.
XX
PT   Selective lysis of bacteria amongst mammalian cells - using 14-mer
PT   or 21 mer lytic peptides
XX
PS   Disclosure; Column 6; 25pp; English.
XX
CC   AAW62920-67 represent minimalist lytic (channel forming) peptides. The
CC   peptides have antibacterial properties in concentrations not lethal
CC   toward mammalian cells. The peptides are heptads (or heptad multimers)
CC   that comprise four nonpolar amino acid residues and three positively
CC   charged amino acid residues, or five nonpolar amino acid residues and
CC   two positively charged amino acid residues. The nonpolar amino acid
CC   residues and the positively charged amino acid residues are distributed
CC   within the heptad such that when the multimer forms an alpha helix the
CC   nonpolar amino acid residues will lie on one face of the alpha-helix,
CC   and the positively charged amino acid residues will lie on the opposite
CC   face of the alpha  helix, whereby the multimer is amphipathic.
XX
SQ   Sequence   21 AA;

  Query Match             75.8%;  Score 50;  DB 19;  Length 21;
  Best Local Similarity   92.3%;  Pred. No. 0.46;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 KALKALLKALKAL 15
              |||||| ||||||
Db          3 KALKALKKALKAL 15


RESULT 22
AAR07738
ID   AAR07738 standard; protein; 29 AA.
XX
AC   AAR07738;
XX
DT   25-MAR-2003  (updated)
DT   22-FEB-1994  (first entry)
XX
DE   Lytic peptide with proliferative activity.
XX
KW   Lytic; neoplastic cells; microbial infections; HIV; [illegible];
KW   wound healing; adjuvant; BRSEF.
XX
OS   synthetic.
```

XX
PN WO9012866 A.
XX
PD 01-NOV-1990.
XX
PF 10-APR-1990; 90WO-US01945.
XX
PR 10-APR-1989; 89US-0336181.
XX
PA (LOUI) UNIV LOUISIANA STATE.
XX
PI Jaynes JM;
XX
DR WPI; 1990-348469/46.
XX
PT New lytic polypeptide(s) with proliferative activity - are
PT alpha helical peptide(s) having aligned amphipathy for treating
PT microbial infections and lysing cancer cells
XX
PS Claim 14; page 40; 57pp; English.
XX
CC This peptide is an analogue of a known lytic peptide. It comprises
CC an alpha helical conformation of amino acids. It is effective at
CC lysing e.g. gram-positive and -negative bacteria and mammalian neo-
CC plastic cells, cells infected with intracellular pathogenic micro-
CC organisms such as HIV. It stimulates the proliferation of fibro-
CC blasts and lymphocytes and can be used in wound healing.
CC See also AAR07744-37, AAR07739-41 and AAR07743-51.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 23 AA;

Query Match 72.7%; Score 48; DB 11; Length 23;
Best Local Similarity 80.0%; Pred. No. 0.8;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FAKALKALLKALKAL 15
|| ||||| |||| |
Db 1 FALALKALKKALKKL 15

RESULT 23
AAR84166
ID AAR84166 standard; Peptide; 23 AA.
XX
AC AAR84166;
XX
DT 06-JUN-1996 (first entry)
XX
DE Peptide enhancer of fibroblast and keratinocyte proliferation.
XX
KW amphipathic peptide; enhancer; fibroblast; keratinocyte; proliferation;
KW wound healing; defensin; antimicrobial.
XX
OS Synthetic.
XX
PN WO9528832 A1.
XX
PD 02-NOV-1995.
XX
PF 19-APR-1995; 95WO-US04718.
XX
PR 20-APR-1994; 94US-0231730.
XX
PA (DEME-) DEMETER BIOTECHNOLOGIES LTD.
XX
PI Jaynes JM, Julian GR;
XX
DR WPI; 1995-382791/49.
XX
PT Use of amphipathic peptide(s) for enhancing fibroblast and
PT keratinocyte proliferation to promote wound healing in a mammal
XX
PS Claim 7; Page 55; 64pp; English.
XX
CC AAR84128-73 are amphipathic peptides which are able to stimulate the
CC proliferative growth of fibroblasts and epithelial cells such as
CC keratinocytes, hence enhancing wound healing in mammalian subjects.
CC The peptides concomitantly have antimicrobial efficacy against
CC microbial species including those which cause or otherwise mediate
CC sepsis and wound infection.
XX
SQ Sequence 23 AA;

Query Match 72.7%; Score 48; DB 11; Length 23;
Best Local Similarity 80.0%; Pred. No. 0.8;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FAKALKALLKALKAL 15
|| ||||| |||| |
Db 1 FALALKALKKALKKL 15

RESULT 24
AAR77080
ID AAR77080 standard; peptide; 23 AA.
XX
AC AAR77080;
XX
DT 20-MAY-1996 (first entry)
XX
DE Synthetic anti neoplastic lytic peptide.
XX
KW Anti cancer; lysis; amphipathic; neoplasia; tumour; cystic fibrosis;
KW bronchopulmonary; viral; virus; malignant; magainin; cecropin;
KW melittin; defensin.
XX
OS Synthetic.
XX
PN WO9527497 A1.
XX
PD 19-OCT-1995.
XX
PF 06-APR-1995; 95WO-US04335.
XX
PR 08-APR-1994; 94US-0225476.
XX
PA (DEME-) DEMETER BIOTECHNOLOGIES LTD.
XX
PI Jaynes JM, Julian GR;
XX
DR WPI; 1995-366226/47.
XX
PT Method of combatting mammalian neoplasias and other disease states
PT by delivering non-naturally occurring, non-cytotoxic lytic
PT proliferative lytic peptide
XX
PS Claim 7; Page 53; 63pp; English.
XX
CC AAR77042-R77081 are synthetic, amphipathic, lytic peptides and are
CC melittin, cecropin, magainin and defensin peptides. The peptides are
CC between 23 and 39 residues long, are amphipathic, carry an overall
CC positive charge and have anti neoplastic activity. The peptides are
CC specifically useful for the lysis of cancer cells. Normal mammalian
CC cells are resistant to lysis due to their highly ordered
CC cytoskeleton, cancerous cells however posses an inherent and
CC structurally compromised cytoskeleton which when acted upon by lytic
CC peptides will cause cell lysis. This activity makes the lytic peptides to be
CC used for in vivo treatment of cancers. The peptides are esp. useful
CC for the treatment of female mammalian cancers e.g. breast, ovarian,
CC uterine and cervical cancers. The peptides can however be used to
CC treat most forms of cancer, cystic fibrosis, pneumonia, bronchial
CC and bronchopulmonary viral and microbial infections.
XX
SQ Sequence 23 AA;

```
  Query Match             72.7%;  Score 48;  DB 16;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.8;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 25
AAR92415
ID   AAR92415 standard; peptide; 23 AA.
XX
AC   AAR92415;
XX
DT   17-SEP-1996  (first entry)
XX
DE   Lytic peptide used in ubiquitin-lytic peptide fusion protein.
XX
KW   Ubiquitin; fusion protein; lysis; infection; neoplasia; wound healing;
KW   stability; reduced toxicity.
XX
OS   Synthetic.
XX
PN   WO9603519-A1.
XX
PD   08-FEB-1996.
XX
PF   24-JUL-1995;   95WO-US09339.
XX
PR   22-JUL-1994;   94US-0279472.
XX
PA   (DEME-) DEMETER BIOTECHNOLOGIES LTD.
PA   (USDA ) US SEC OF AGRIC.
XX
PI   Belknap W,  Garbarino J,  Jaynes J;
XX
DR   WPI; 1996-117061/12.
XX
PT   New fusion protein of ubiquitin and a lytic peptide - for treating
PT   infections and neoplasia, healing wounds, etc. also related nucleic
PT   acid, vectors, and transformed cells
XX
PS   Claim 5; Page 23; 112pp; English.
XX
CC   AAR92372-R92462 are lytic peptides used to create ubiquitin-lytic
CC   peptide fusion proteins in which the ubiquitin polypeptide is linked
CC   at its 3' terminus to the lytic peptide. The lytic peptides are pref.
CC   selected from either the cecropins, defensins, sarcotoxins, melittin
CC   and magainins. The fusion proteins (FPs) are useful for treating
CC   protozoal, bacterial, fungal and viral infections and neoplasia (in
CC   plants and animals) in the same way as the FP alone, they also
CC   promote wound healing. FPs produced in bacteria may be cleaved in
CC   vitro by ubiquitin hydrolases to recover the active lytic peptide.
CC   FPs produced in eukaryotic cells are cleaved by endogenous enzymes
CC   to yield lytic peptide. Recombinant DNA encoding the FPs have
CC   greater stability in bacteria than DNA encoding the lytic peptide
CC   only.
XX
SQ   Sequence   23 AA;

  Query Match             72.7%;  Score 48;  DB 17;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.8;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 26
AAR89972
ID   AAR89972 standard; peptide; 23 AA.
XX
AC   AAR89972;
XX
DT   16-SEP-1996  (first entry)
XX
DE   Synthetic lytic peptide #6.
XX
KW   Lytic peptide; ubiquitin; synthetic analogues; cell membrane;
KW   microbial pathogen; disease resistant plant; bacteria; infection;
KW   protozoa; virus; neoplasia; fusion protein; hydrolase.
XX
OS   Synthetic.
XX
PN   WO9603522-A1.
XX
PD   08-FEB-1996.
XX
PF   24-JUL-1995;   95WO-US09338.
XX
PR   22-JUL-1994;   94US-0279472.
XX
PA   (DEME-) DEMETER BIOTECHNOLOGIES LTD.
XX
PI   Jaynes J;
XX
DR   WPI; 1996-117064/12.
XX
PT   Lytic peptide(s), useful for developing disease resistant plants
PT   can be expressed as fusion protein with ubiquitin for stable prod.
PT   in bacterial host cells
XX
PS   Claim 1; Page 71; 111pp; English.
XX
CC   AAR89967-R90021 and AAR90726-R90764 represent synthetic analogues of
CC   naturally occurring lytic peptides.  Lytic peptides destroy prokaryotic
CC   and other non-host cells by disrupting the cell membrane and promoting
CC   cell lysis.  Synthetic lytic peptide analogues have similar or higher
CC   levels of lytic activity for many different types of cells compared to
CC   naturally occurring forms.  The concentration of the synthetic analogue
CC   required to lyse microbial pathogens does not cause damage to animal
CC   cells.  The lytic peptides can be expressed in plants to allow for the
CC   development of disease resistant plants.  The peptides are useful in
CC   promoting wound healing and combatting bacterial, fungal, protozoal,
CC   The lytic peptides can also be used for combatting plant, animal,
CC   viral or bacterial infections or neoplasias in mammals or plants.
CC   Lytic peptide ubiquitin fusion proteins are stable in prokaryotic
CC   bacterial hosts.  Bacteria lack the hydrolase which cleaves the peptide
CC   from ubiquitin, and therefore the active (and toxic) lytic peptide
CC   will not be released in the host cells.  The recombinant product
CC   lytic peptide can be retrieved from the fusion protein by cleavage in
CC   vitro.
XX
SQ   Sequence   23 AA;

  Query Match             72.7%;  Score 48;  DB 17;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.8;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 27
AAW76374
ID   AAW76374 standard; peptide; 23 AA.
XX
AC   AAW76374;
XX
DT   04-DEC-1998  (first entry)
XX
DE   Rat hecate peptide.
XX
```

KW GnHR; lytic peptide; rat; gonadotrophin-releasing hormone; contraception;
KW sterility; luteinising hormone, LH, 1 LHRH-III, fertility, pituitary;
KW lamprey-luteinising hormone-releasing hormone, gonadotropes; inhibitor;
KW tumour; ligand; fusion protein; reproductive capacity; insect; treatment;
KW growth rate; pest control, L hecate, cancer; adenoma; lymphocyte;
KW autoimmune disease.
XX
OS Rattus sp.
XX
PN WO9842365-A1.
XX
PD 01-OCT-1998.
XX
PF 27-MAR-1998; 98WO-US06114.
XX
PR 03-SEP-1997; 97US-0057456.
PR 27-MAR-1997; 97US-0041009.
PR 04-JUN-1997; 97US-0869153.
XX
PA (LOUU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
XX
PI Elzer PH, Enright FM, Foil LD, Hansel W, Jaynes JM;
PI Koonce KL, McCann SM, Melrose PA, Yu WH;
XX
DR WPI; 1998-531711/45.
XX
PT New fusion of hormone and lytic peptide for selective cell killing -
PT particularly for controlling fertility in animals, insect pests,
PT fish etc., also for treatment of hormone-dependent cancer, viral
PT infections and auto-immune diseases
XX
PS Example 1 6; Page 37; 59pp; English.
XX
CC This sequence represents the rat hecate peptide which is used in a method
CC for producing long-term contraception or sterility by administering
CC gonadotrophin-releasing hormone (GnRH), beta luteinising hormone (LH) or
CC lamprey-luteinising hormone-releasing hormone (1 LHRH III) or temporarily
CC restoring fertility in a mammal in which the pituitary gonadotropes have
CC been selectively destroyed by administration of GnRH or 1-LHRH-III. This
CC sequence also has applications in methods for killing, or inhibiting
CC growth of hormone- or ligand-dependent tumours by administering the
CC relevant hormone or ligand plus a lytic peptide, for killing a cell the
CC activity of which is dependent on binding of a cell-surface receptor to
CC a ligand by administering the ligand and lytic peptide, inhibiting
CC reproductive capacity of an insect by administration of a lytic peptide.
CC Fusion proteins combining such proteins and lytic peptides can be fused
CC and may also include a carrier domain, specifically vitamin B12, that
CC facilitates intestinal uptake after oral administration. These methods
CC have applications for increasing the growth rate of mammals, for pest
CC control e.g. plants containing an exogenous gene encoding L-hecate. A
CC further application is in the treatment of ovarian, breast, prostate,
CC endometrial or testicular cancers, prolactinoma, growth hormone-,
CC thyrotropin- or gonadotropin-dependent adenomas, or any pituitary
CC adenoma. In addition the proteins can be used to kill lymphocytes
CC involved in a wide range of autoimmune diseases or to destroy
CC virus-infected cells.
XX
SQ Sequence 23 AA;

Query Match 72.7%; Score 48; DB 19; Length 23;
Best Local Similarity 80.0%; Pred. No. 0.8;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FAKALKALLKALKAL 15
|| ||||| |||| |
Db 1 FALALKALKKALKKL 15

RESULT 28
AAW39786
ID AAW39786 standard; peptide; 23 AA.
XX
AC AAW39786;
XX
DT 20-MAY-1998 (first entry)
XX
DE Synthetic peptide DP-1.
XX
KW Lytic peptide; lysine-rich; proteolytic digestion; methylation; trypsin;
KW protection; amphipathic alpha-helix; beta-pleated sheet; treatment;
KW infection; viral; bacterial; yeast; fungal; protozoan; cancer; DP-1.
XX
OS Synthetic.
XX
PN US5717064-A.
XX
PD 10-FEB-1998.
XX
PF 24-APR-1995; 95US-0427001.
XX
PR 24-APR-1995; 95US-0427001.
PR 18-NOV-1993; 93US-0148889.
XX
PA (DEME-) DEMETER BIOTECHNOLOGIES LTD.
XX
PI Jaynes JM, Julian GR;
XX
DR WPI; 1998-158370/14.
XX
PT Cytolytic peptide analoques - with methylated lysine residues to
PT increase protease resistance
XX
PS Example 2; Column 9; 21pp; English.
XX
CC Peptide AAW39786 (also known as DP-1) is used as a test substrate in a
CC reductive alkylation reaction used in the analysis of a family of
CC synthetic lytic peptides which are stabilised by having methylated
CC epsilon -amino groups at their lysine residues (see AAW39750-W39785).
CC Peptides AAW39750-W39771 and AAW39781 W39785 have an amphipathic
CC alpha-helix conformation while peptides AAW39772 W39780 have a
CC beta-pleated sheet conformation. These peptides have enhanced resistance
CC to proteolytic digestion by trypsin. Such peptides can be used to treat
CC infections by lysing bacterial, yeast, fungal and protozoan cells or to
CC treat cancers by lysing neoplastic or transformed cells. They can also be
CC used to treat viral infections by lysing enveloped viruses and
CC virus-infected cells.
XX
SQ Sequence 23 AA;

Query Match 72.7%; Score 48; DB 19; Length 23;
Best Local Similarity 80.0%; Pred. No. 0.8;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FAKALKALLKALKAL 15
|| ||||| |||| |
Db 1 FALALKALKKALKKL 15

RESULT 29
AAY03857
ID AAY03857 standard; peptide; 23 AA.
XX
AC AAY03857;
XX
DT 16-JUN-1999 (first entry)
XX
DE Amino acid sequence of a lytic peptide hecate.
XX
KW Contraception; sterility; amphipathic; lytic peptide; hormone domain;
KW gonadotropin-releasing hormone; GnRH; analogue; gonadotrope; deer; ox;
KW cow; bull; pig; horse; sheep.
XX
OS Synthetic.
XX
PN WO9911282-A1.
XX

PD 11-MAR-1999.
XX
PF 01-SEP-1998; 98WO-US18117.
XX
PR 03-SEP-1997; 97US-0057456.
XX
PA (LOUU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
XX
PI Elzer PH, Enright F, Hansel W, Jaynes JM, Melrose PA;
XX
DR WPI; 1999-204980/17.
XX
PT Production of long-term contraception or sterility in, e.g. cats -
PT by administering a compound comprising fusion peptide of
PT gonadotropin-releasing hormone and lytic peptide domains
XX
PS Examples 1-6; Page 23; 34pp; English.
XX
CC The invention relates to method for producing long-term contraception
CC or sterility in a mammal that comprises administering an amphipathic
CC lytic peptide compound. The compounds comprise: (a) a hormone domain
CC selected from gonadotropin-releasing hormone (GnRH) and GnRH analogues,
CC and (b) a lytic peptide domain. The compounds are relatively small and
CC are not antigenic. Lysis of gonadotropes has been observed to be very
CC rapid. The components: the ligand and the lytic peptide-may optionally
CC be administered as a fusion peptide. The methods can be applied to dogs,
CC cats, cows, bulls, pigs, horses, sheep or humans, including sexually
CC immature individuals.
XX
SQ Sequence 23 AA;

Query Match 72.7%; Score 48; DB 20; Length 23;
Best Local Similarity 80.0%; Pred. No. 0.8;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FAKALKALLKALKAL 15
|| ||||| |||| |
Db 1 FALALKALKKALKKL 15

RESULT 30
AAW84279
ID AAW84279 standard; peptide; 23 AA.
XX
AC AAW84279;
XX
DT 17-MAR-1999 (first entry)
XX
DE Lytic peptide bocato
XX
KW Hormone domain; gonadotropin releasing hormone; GnRH;
KW luteinising hormone releasing hormone; LHRH-III; estrogen;
KW testosterone; luteinising hormone; chorionic gonadotropin;
KW follicle stimulating hormone; melanocyte-stimulating hormone; estradiol;
KW dopamine; somatostatin; lytic peptide; long term contraception;
KW sterilisation; human; fish; insect; hormone-dependent tumour;
KW hormone-related disease; autoimmune disorder; treatment.
XX
OS Synthetic.
XX
PN WO9842364-A1.
XX
PD 01-OCT-1998.
XX
PF 26-MAR-1998; 98WO-US06015.
XX
PR 03-SEP-1997; 97US-0057456.
PR 27-MAR-1997; 97US-0041009.
PR 04-JUN-1997; 97US-0869154.
XX
PA (DEME) DEMETER BIOTECHNOLOGIES LTD.
PA (LOUU) UNIV LOUISIANA STATE & AGRIC.
XX
PI Enright FM, Foil LD, Hansel WB, Jaynes JM, Melrose PA.
XX
DR WPI; 1999-070063/06.
XX
PT New hormone-lytic peptide compounds - used in long term
PT contraception or sterilisation, for killing insect or tumour
PT infected cells or for treating tumours or autoimmune disorders
XX
PS Example 3; Page 46; 48pp; English.
XX
CC The present sequence represents a lytic peptide. The peptide is
CC used in a compound in conjunction with the hormone luteinising
CC releasing hormone (GnRH), or luteinising hormone releasing hormone
CC (LHRH) III, estrogen, testosterone, luteinising hormone, chorionic
CC gonadotropin, follicle stimulating hormone, melanocyte-stimulating
CC hormone, estradiol, dopamine, somatostatin and analogues. These
CC hormones. The compounds can be used for sterilisation of animals
CC that are driven by or are dependent on sperm. The compounds
CC They can be used for providing long term contraception
CC in humans, domesticated or wild mammals, birds, reptiles, crustacea
CC bony fish, cartilaginous fish, jawless fish, and amphibians. The
CC insects or molluscs. They can also be used for inhibiting the
CC malignant and non malignant hormone dependent tumours
CC other hormone related diseases, for selectively killing infected
CC cells or for treating autoimmune disorders.
XX
SQ Sequence 23 AA;

Query Match 72.7%; Score 48; DB 20; Length 23;
Best Local Similarity 80.0%; Pred. No. 0.8;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FAKALKALLKALKAL 15
|| ||||| |||| |
Db 1 FALALKALKKALKKL 15

RESULT 31
ABR00760
ID ABR00760 standard; peptide; 23 AA.
XX
AC ABR00760;
XX
DT 03-APR-2003 (first entry)
XX
DE Bioactive synthetic peptide Bocato AM.
XX
KW Antibacterial; fungicide; cytostatic; vulnerary; [illegible]
KW gram+ve; antimycotic; human fibroblast; human lymph; [illegible]
KW bioactive.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 23
FT /note= "C-terminal amide"
XX
PN WO200279408-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009134.
XX
PR 28-MAR-2001; 2001US-279509P.
PR 28-MAR-2001; 2001US-08200553.
XX
PA (HELI) HELIX BIOMEDIX INC.
XX
PI Owen DR;
XX
DR WPI; 2003-221247/21.
XX
PT New isolated peptide for treating cancer, [illegible]

PT acne, inhibiting growth of microbial cells, or promoting proliferation
PT of cells, comprises phenylalanine, leucine, alanine or lysine residues
PT -
XX
PS Claim 7; Page 5; 133pp; English.
XX
CC The invention relates to a novel isolated peptide which is 5-23 amino
CC acids in length, and comprising phenylalanine, leucine, alanine or lysine
CC residues, or contains at least 50 % of the residues. The peptides of the
CC invention have antibacterial, fungicide, cytostatic, and vulnerary
CC activity. The peptides are useful in treating cancer, cystic fibrosis or
CC acne, inhibiting the growth of microbial cells, promoting the
CC stimulation and/or proliferation of human fibroblasts and lymphocytes,
CC promoting wound healing, and in enhancing the activity of a therapeutic
CC agent. The sequences shown in ABR00759-ABR00923 represent the bioactive
CC peptides of the invention.
XX
SQ Sequence 23 AA;

Query Match 72.7%; Score 48; DB 24; Length 23;
Best Local Similarity 80.0%; Pred. No. 0.8;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FAKALKALLKALKAL 15
|| ||||| |||| |
Db 1 FALALKALKKALKKL 15

RESULT 32
ABR00945
ID ABR00945 standard; peptide; 23 AA.
XX
AC ABR00945;
XX
DT 03-APR-2003 (first entry)
XX
DE Bioactive synthetic peptide Hecate AC #1010.
XX
KW Antibacterial; fungicide; cytostatic; vulnerary; cancer; cystic fibrosis;
KW acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
KW bioactive.
XX
OS Synthetic.
XX
PN WO200279408-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US09534.
XX
PR 28-MAR-2001; 2001US-279505P.
PR 28-MAR-2001; 2001US-0820053.
XX
PA (HELI-) HELIX BIOMEDIX INC.
XX
PI Owen DR;
XX
DR WPI; 2003-221247/21.
XX
PT New isolated peptide for treating cancer, cystic fibrosis, wounds or
PT acne, inhibiting growth of microbial cells, or promoting proliferation
PT of cells, comprises phenylalanine, leucine, alanine or lysine residues
PT
XX
PS Claim 7; Page 5; 133pp; English.
XX
CC The invention relates to a novel isolated peptide which is 5-23 amino
CC acids in length, and comprising phenylalanine, leucine, alanine or lysine
CC residues, or contains at least 50 % of the residues. The peptides of the
CC invention have antibacterial, fungicide, cytostatic, and vulnerary
CC activity. The peptides are useful in treating cancer, cystic fibrosis or
CC acne, inhibiting the growth of microbial cells, promoting the
CC stimulation and/or proliferation of human fibroblasts and lymphocytes,
CC promoting wound healing, and in enhancing the activity of a therapeutic
CC agent. The sequences shown in ABR00759-ABR00923 represent the bioactive
CC peptides of the invention.
XX
SQ Sequence 23 AA;

Query Match 72.7%; Score 48; DB 24; Length 23;
Best Local Similarity 80.0%; Pred. No. 0.8;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FAKALKALLKALKAL 15
|| ||||| |||| |
Db 1 FALALKALKKALKKL 15

RESULT 33
AAW07282
ID AAW07282 standard; peptide; 18 AA.
XX
AC AAW07282;
XX
DT 29-MAY-1997 (first entry)
XX
DE Amphiphilic antimicrobial peptide MB 41.
XX
KW amphiphilic antimicrobial; log kill; Staphylococcus aureus; charge;
KW Escherichia coli; vectorial analysis; hydrophilic-lipophilic balance;
KW hydrophobic moment; equation; antimicrobial; antibacterial;
KW antifungal; disinfection; spoilage prevention; preservation.
XX
OS Synthetic.
XX
PN WO9628468-A2.
XX
PD 19-SEP-1996.
XX
PF 27-FEB-1996; 96WO-EP00844.
XX
PR 09-MAR-1995; 95GB-0004761.
XX
PA (UNIL) UNILEVER NV.
PA (UNIL) UNILEVER PLC.
XX
PI Bhakoo M, Patel S, Stott PJ;
XX
DR WPI; 1996-433760/43.
XX
PT New amphiphilic antimicrobial peptide(s) - having particular
PT combinations of hydrophilic and hydrophobic amino acid residues
XX
PS Example -; Page 22; 39pp; English.
XX
CC AAW07279-90 examples of amphiphilic antimicrobial peptides for
CC comparison to claimed amphiphilic antimicrobial peptides (AAW07257-9),
CC and show that relatively minor changes in structure can have significant
CC consequences as regards the antimicrobial activity of the molecules. The
CC log kills were predicted against S. aureus and against E. coli, and
CC values of more than 5 and 4 respectively, correspond to greater
CC antimicrobial activity. Effective antimicrobial peptides are
CC discriminated from ineffective peptides by a vectorial analysis in
CC dimensions corresponding to charge, hydrophilic/lipophilic balance,
CC hydrophobic moment and amphiphilicity of the peptides, where effective
CC peptides fall into the region which is anti-clockwise of the
CC amphiphilicity dimension and clockwise of the charge dimension.
CC Effective peptides are further discriminated from ineffective peptides by
CC means of an equation relating certain physical properties of the peptides
CC to their biological activity against specific microorganisms. The
CC peptides can be used in antimicrobial, preservative or antifungal
CC compsns. They can be used for the disinfection of surfaces, spoilage
CC prevention, preservation or other hygiene processes.
XX
SQ Sequence 18 AA;

```
  Query Match             65.2%;  Score 43;  DB 17;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.6;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 KALKALLKALKA 14
              |||||| |||| :
Db          5 KALKALKKALKS 16


RESULT 34
AAM49118
ID   AAM49118 standard; peptide; 23 AA.
XX
AC   AAM49118;
XX
DT   20-MAY-2002  (first entry)
XX
DE   Cationic amphipathic gene transfer vector peptide, RAWA.
XX
KW   Cationic; amphipathic; gene transfer vector; gene therapy; non-viral;
KW   nucleic acid carrier; RAWA.
XX
OS   Synthetic.
XX
PN   WO200210197-A1.
XX
PD   07-FEB-2002.
XX
PF   06-JUL-2001; 2001WO-ES00274.
XX
PR   20-JUL-2000; 2000ES-0001806.
XX
PA   (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
PA   (MEDP-) MEDPLANT GENETICS SL.
PA   (JESU ) JESUS FOMINAYA GUTIERREZ.
PA   (BUEL/) SIMON BUELA I.
XX
PI   Fominaya Gutierrez J,  Bernad Miana A,  Gasset Vega MA;
XX
DR   WPI; 2002-257378/30.
XX
PT   New cationic amphipathic peptide, useful as carrier for nucleic acid,
PT   e.g. in gene therapy, binds to, and condenses, nucleic acid and
PT   destabilizes cellular membranes
XX
PS   Claim 5; Page 41; 54pp; Spanish.
XX
CC   The invention relates to novel cationic amphipathic peptides of the
CC   general formula:
CC   X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-X17-X18-X19-X20
CC   X21-X22-X23 where:
CC   X1, X5, X9, X12, X19 and X23 are Arg, Lys or ornithine;
CC   and all other Xs are independently selected from Gly, Ala,
CC   Val, Leu, Ile, Trp, Tyr or Phe, with X3 preferably being an aromatic
CC   amino acid, particularly Trp. The constituent amino acids of the
CC   peptide may be L- or D-form, and in a particular embodiment, all
CC   residues are D-form. The peptides of the invention are able to
CC   simultaneously bind to nucleic acid and to disrupt biological
CC   membranes and may thus be used as carriers for nucleic acids,
CC   particularly to prepare non-viral gene transfer vectors for gene
CC   therapy or for experimental transfection. Such vectors based on
CC   peptides of the invention are not inhibited by serum. Compared with
CC   similar known peptides, such as KALA (AAM49119), the peptides of the
CC   invention have an increased capacity for condensing genetic material,
CC   have lower cytotoxicity and provide more efficient transfer of
CC   genetic material. The present sequence represents a specifically
CC   claimed peptide of the invention designated RAWA.
XX
SQ   Sequence   23 AA;

  Query Match             65.2%;  Score 43;  DB 23;  Length 23;
  Best Local Similarity   64.3%;  Pred. No. 4.6;
  Matches    9;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              :|:|:|| :|:|:|
Db          8 AKALKALAKALKAL 21


RESULT 35
ABR00767
ID   ABR00767 standard; peptide; 23 AA.
XX
AC   ABR00767;
XX
DT   03-APR-2003  (first entry)
XX
DE   Bioactive synthetic peptide FLAK03 AM.
XX
KW   Antibacterial; fungicide; cytostatic; vulnerary; cancer; cytostatic;
KW   gene; antimicrobial; human like blood; human lymph; wound healing;
KW   bioactive.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified site   23
FT                   /note= "C terminal amide"
XX
PN   WO200279408-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US09054.
XX
PR   28-MAR-2001; 2001US-279057P.
PR   28-MAR-2001; 2001US-0820053.
XX
PA   (BEIA ) BEIA-MEDIX INC.
XX
PI   Owen DR;
XX
DR   WPI; 2003-221247/21.
XX
PT   New isolated peptide for treating cancer, cytostatic, vulnerary, gene,
PT   gene, inhibiting growth of microbial cells, or promoting proliferation
PT   of cells, comprises phenylalanine, leucine, arginine or lysine residues
PT   .
XX
PS   Example 2; Page 5; 133pp; English.
XX
CC   The invention relates to a novel isolated peptide (I) having 5-25
CC   acids in length, and comprising phenylalanine, leucine, arginine
CC   residues, or contains at least 50 % of the residues. The peptide
CC   invention have antibacterial, fungicide, cytostatic and vulnerary
CC   activity. The peptides are useful in treating cancer, cytostatic,
CC   gene, inhibiting the growth of microbial cells, promoting
CC   stimulation and/or proliferation of human cells, e.g. fibroblasts,
CC   promoting wound healing, and in cosmetics. The present sequence is a
CC   agent. The sequences shown in ABR00765-ABR00768 represent specific
CC   peptides of the invention.
XX
SQ   Sequence   23 AA;

  Query Match             65.2%;  Score 43;  DB 24;  Length 23;
  Best Local Similarity   73.9%;  Pred. No. 4.6;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FAKAAKALLKALKAL 15
              || ||||| | || |
Db          1 FALALKALKKLLKKL 15


RESULT 36
ABR00777
ID   ABR00777 standard; peptide; 23 AA.
```

```
XX
AC   ABR00777;
XX
DT   03-APR 2003  (first entry)
XX
DE   Bioactive synthetic peptide Hecate 2DAc.
XX
KW   Antibacterial; fungicide; cytostatic; vulnerary; cancer; cystic fibrosis;
KW   acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
KW   bioactive.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   13
FT                   /note  "D-form residue"
FT   Modified-site   14
FT                   /note  "D-form residue"
XX
PN   WO200279408 A2.
XX
PD   10-OCT 2002.
XX
PF   28-MAR-2002; 2002WO-US09534.
XX
PR   28-MAR-2001; 2001US-279505P.
PR   28-MAR 2001; 2001US-0820053.
XX
PA   (HELI ) HELIX BIOMEDIX INC.
XX
PI   Owen DR;
XX
DR   WPI; 2003-221247/21.
XX
PT   New isolated peptide for treating cancer, cystic fibrosis, wounds or
PT   acne, inhibiting growth of microbial cells, or promoting proliferation
PT   of cells, comprises phenylalanine, leucine, alanine or lysine residues
PT
XX
PS   Claim 7; Page 6; 133pp; English.
XX
CC   The invention relates to a novel isolated peptide which is 5-23 amino
CC   acids in length, and comprising phenylalanine, leucine, alanine or lysine
CC   residues, or contains at least 50 % of the residues. The peptides of the
CC   invention have antibacterial, fungicide, cytostatic, and vulnerary
CC   activity. The peptides are useful in treating cancer, cystic fibrosis or
CC   acne, inhibiting the growth of microbial cells, promoting the
CC   stimulation and/or proliferation of human fibroblasts and lymphocytes,
CC   promoting wound healing, and in enhancing the activity of a therapeutic
CC   agent. The sequences shown in ABR00759-ABR00923 represent the bioactive
CC   peptides of the invention.
XX
SQ   Sequence   23 AA;

  Query Match             65.2%;  Score 43;  DB 24;  Length 23;
  Best Local Similarity   73.3%;  Pred. No. 4.6;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALEALLKALEAL 15
              || |||||  ||| |
Db          1 FALALKALKKALXXI 15


RESULT 37
ABR00770
ID   ABR00770 standard; peptide; 19 AA.
XX
AC   ABR00770;
XX
DT   03-APR 2003  (first entry)
XX
DE   Bioactive synthetic peptide FLAK06 AM.
XX
KW   Antibacterial; fungicide; cytostatic; vulnerary; cancer; cystic fibrosis;
KW   acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
KW   bioactive.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   19
FT                   /note  "C-terminal amide"
XX
PN   WO200279408 A2.
XX
PD   10-OCT 2002.
XX
PF   28-MAR-2002; 2002WO-US09534.
XX
PR   28-MAR-2001; 2001US-279505P.
PR   28-MAR 2001; 2001US-0820053.
XX
PA   (HELI ) HELIX BIOMEDIX INC.
XX
PI   Owen DR;
XX
DR   WPI; 2003-221247/21.
XX
PT   New isolated peptide for treating cancer, cystic fibrosis, wounds or
PT   acne, inhibiting growth of microbial cells, or promoting proliferation
PT   of cells, comprises phenylalanine, leucine, alanine or lysine residues
PT
XX
PS   Claim 7; Page 5; 133pp; English.
XX
CC   The invention relates to a novel isolated peptide which is 5-23 amino
CC   acids in length, and comprising phenylalanine, leucine, alanine or lysine
CC   residues, or contains at least 50 % of the residues. The peptides of the
CC   invention have antibacterial, fungicide, cytostatic, and vulnerary
CC   activity. The peptides are useful in treating cancer, cystic fibrosis or
CC   acne, inhibiting the growth of microbial cells, promoting the
CC   stimulation and/or proliferation of human fibroblasts and lymphocytes,
CC   promoting wound healing, and in enhancing the activity of a therapeutic
CC   agent. The sequences shown in ABR00759-ABR00923 represent the bioactive
CC   peptides of the invention.
XX
SQ   Sequence   19 AA;

  Query Match             65.2%;  Score 43;  DB 24;  Length 19;
  Best Local Similarity   73.3%;  Pred. No. 5.4;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALEALLKALEAL 15
              || |||||  ||| |
Db          1 FALALKALKKLLKAL 15


RESULT 38
ABR00771
ID   ABR00771 standard; peptide; 19 AA.
XX
AC   ABR00771;
XX
DT   03-APR 2003  (first entry)
XX
DE   Bioactive synthetic peptide FLAK06 AC.
XX
KW   Antibacterial; fungicide; cytostatic; vulnerary; cancer; cystic fibrosis;
KW   acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
KW   bioactive.
XX
OS   Synthetic.
XX
PN   WO200279408 A2.
XX
PD   10-OCT 2002.
```

```
XX
PF   28 MAR 2002; 2002WO-US009534.
XX
PR   28-MAR 2001; 2001US-279505P.
PR   28-MAR 2001; 2001US-0820053.
XX
PA   (HELI ) HELIX BIOMEDIX INC.
XX
PI   Owen DR;
XX
DR   WPI; 2003-221247/21.
XX
PT   New isolated peptide for treating cancer, cystic fibrosis, wounds or
PT   acne, inhibiting growth of microbial cells, or promoting proliferation
PT   of cells, comprises phenylalanine, leucine, alanine or lysine residues
PT
XX
PS   Claim 7; Page 5; 133pp; English.
XX
CC   The invention relates to a novel isolated peptide which is 5-23 amino
CC   acids in length, and comprising phenylalanine, leucine, alanine or lysine
CC   residues, or contains at least 50 % of the residues. The peptides of the
CC   invention have antibacterial, fungicide, cytostatic, and vulnerary
CC   activity. The peptides are useful in treating cancer, cystic fibrosis or
CC   acne, inhibiting the growth of microbial cells, promoting the
CC   stimulation and/or proliferation of human fibroblasts and lymphocytes,
CC   promoting wound healing, and in enhancing the activity of a therapeutic
CC   agent. The sequences shown in ABR00759-ABR00923 represent the bioactive
CC   peptides of the invention.
XX
SQ   Sequence   19 AA;

  Query Match             63.6%;  Score 42;  DB 24;  Length 19;
  Best Local Similarity   73.3%;  Pred. No. 5.4;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |  |||
Db          1 FALALKALKKLKKAL 15


RESULT 39
ABR00826
ID   ABR00826 standard; peptide; 20 AA.
XX
AC   ABR00826;
XX
DT   03-APR-2003  (first entry)
XX
DE   Bioactive synthetic peptide CA(1-8)Melittin(11/23).
XX
KW   Antibacterial; fungicide; cytostatic; vulnerary; cancer; cystic fibrosis;
KW   acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
KW   bioactive.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   20
FT                   /note= "C-terminal amide"
XX
PN   WO2002079408-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US009534.
XX
PR   28-MAR-2001; 2001US-279505P.
PR   28-MAR-2001; 2001US-0820053.
XX
PA   (HELI-) HELIX BIOMEDIX INC.
XX
PI   Owen DR;
XX
DR   WPI; 2003-221247/21.
XX
PT   New isolated peptide for treating cancer, cystic fibrosis, wounds or
PT   acne, inhibiting growth of microbial cells, or promoting proliferation
PT   of cells, comprises phenylalanine, leucine, alanine or lysine residues
PT
XX
PS   Claim 7; Page 7; 133pp; English.
XX
CC   The invention relates to a novel isolated peptide which is 5-23 amino
CC   acids in length, and comprising phenylalanine, leucine, alanine or lysine
CC   residues, or contains at least 50 % of the residues. The peptides of the
CC   invention have antibacterial, fungicide, cytostatic, and vulnerary
CC   activity. The peptides are useful in treating cancer, cystic fibrosis or
CC   acne, inhibiting the growth of microbial cells, promoting the
CC   stimulation and/or proliferation of human fibroblasts and lymphocytes,
CC   promoting wound healing, and in enhancing the activity of a therapeutic
CC   agent. The sequences shown in ABR00759-ABR00923 represent the bioactive
CC   peptides of the invention.
XX
SQ   Sequence   20 AA;

  Query Match             63.6%;  Score 42;  DB 24;  Length 20;
  Best Local Similarity   73.3%;  Pred. No. 5.4;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||||| |  |||
Db          1 FALALKALKKLKKAL 15


RESULT 40
ABR00723
ID   ABR00723 standard; peptide; 23 AA.
XX
AC   ABR00723;
XX
DT   03-APR-2003  (first entry)
XX
DE   Bioactive synthetic peptide KAL V.
XX
KW   Antibacterial; fungicide; cytostatic; vulnerary; cancer; cystic fibrosis;
KW   acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
KW   bioactive.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   23
FT                   /note= "C-terminal amide"
XX
PN   WO2002079408-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US009534.
XX
PR   28-MAR-2001; 2001US-279505P.
PR   28-MAR-2001; 2001US-0820053.
XX
PA   (HELI ) HELIX BIOMEDIX INC.
XX
PI   Owen DR;
XX
DR   WPI; 2003-221247/21.
XX
PT   New isolated peptide for treating cancer, cystic fibrosis, wounds or
PT   acne, inhibiting growth of microbial cells, or promoting proliferation
PT   of cells, comprises phenylalanine, leucine, alanine or lysine residues
PT
XX
PS   Claim 7; Page 5; 133pp; English.
```

```
XX
CC   The invention relates to a novel isolated peptide which is 5-23 amino
CC   acids in length, and comprising phenylalanine, leucine, alanine or lysine
CC   residues, or contains at least 50 % of the residues. The peptides of the
CC   invention have antibacterial, fungicide, cytostatic, and vulnerary
CC   activity. The peptides are useful in treating cancer, cystic fibrosis or
CC   acne, inhibiting the growth of microbial cells, promoting the
CC   stimulation and/or proliferation of human fibroblasts and lymphocytes,
CC   promoting wound healing, and in enhancing the activity of a therapeutic
CC   agent. The sequences shown in ABR00759 ABR00923 represent the bioactive
CC   peptides of the invention.
XX
SQ   Sequence   23 AA;

  Query Match             63.6%;  Score 42;  DB 24;  Length 23;
  Best Local Similarity   78.6%;  Pred. No. 6.5;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              | ||||| |||| |
Db          2 ALALKALKKALKKL 15


RESULT 41
ABR00916
ID   ABR00916 standard; peptide; 23 AA.
XX
AC   ABR00916;
XX
DT   03-APR-2003  (first entry)
XX
DE   Bioactive synthetic peptide HECATE AMV.
XX
KW   Antibacterial; fungicide; cytostatic; vulnerary; cancer; cystic fibrosis;
KW   acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
KW   bioactive.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   23
FT                   /note= "C-terminal amide"
XX
PN   WO200279408 A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US09534.
XX
PR   28-MAR-2001; 2001US-279505P.
PR   28-MAR-2001; 2001US-0820053.
XX
PA   (HELI-) HELIX BIOMEDIX INC.
XX
PI   Owen DR;
XX
DR   WPI; 2003-221247/21.
XX
PT   New isolated peptide for treating cancer, cystic fibrosis, wounds or
PT   acne, inhibiting growth of microbial cells, or promoting proliferation
PT   of cells, comprises phenylalanine, leucine, alanine or lysine residues
PT
XX
PS   Example 2; Page 9; 133pp; English.
XX
CC   The invention relates to a novel isolated peptide which is 5-23 amino
CC   acids in length, and comprising phenylalanine, leucine, alanine or lysine
CC   residues, or contains at least 50 % of the residues. The peptides of the
CC   invention have antibacterial, fungicide, cytostatic, and vulnerary
CC   activity. The peptides are useful in treating cancer, cystic fibrosis or
CC   acne, inhibiting the growth of microbial cells, promoting the
CC   stimulation and/or proliferation of human fibroblasts and lymphocytes,
CC   promoting wound healing, and in enhancing the activity of a therapeutic
CC   agent. The sequences shown in ABR00759-ABR00923 represent the bioactive
CC   peptides of the invention.
XX
SQ   Sequence   23 AA;

  Query Match             63.6%;  Score 42;  DB 24;  Length 23;
  Best Local Similarity   78.6%;  Pred. No. 6.5;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              | ||||| |||| |
Db          2 ALALKALKKALKKL 15


RESULT 42
ABR00917
ID   ABR00917 standard; peptide; 23 AA.
XX
AC   ABR00917;
XX
DT   03-APR-2003  (first entry)
XX
DE   Bioactive synthetic peptide HECATE ACV.
XX
KW   Antibacterial; fungicide; cytostatic; vulnerary; cancer; cystic fibrosis;
KW   acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
KW   bioactive.
XX
OS   Synthetic.
XX
PN   WO200279408 A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US09534.
XX
PR   28-MAR-2001; 2001US-279505P.
PR   28-MAR-2001; 2001US-0820053.
XX
PA   (HELI-) HELIX BIOMEDIX INC.
XX
PI   Owen DR;
XX
DR   WPI; 2003-221247/21.
XX
PT   New isolated peptide for treating cancer, cystic fibrosis, wounds or
PT   acne, inhibiting growth of microbial cells, or promoting proliferation
PT   of cells, comprises phenylalanine, leucine, alanine or lysine residues
PT
XX
PS   Claim 7; Page 9; 133pp; English.
XX
CC   The invention relates to a novel isolated peptide which is 5-23 amino
CC   acids in length, and comprising phenylalanine, leucine, alanine or lysine
CC   residues, or contains at least 50 % of the residues. The peptides of the
CC   invention have antibacterial, fungicide, cytostatic, and vulnerary
CC   activity. The peptides are useful in treating cancer, cystic fibrosis or
CC   acne, inhibiting the growth of microbial cells, promoting the
CC   stimulation and/or proliferation of human fibroblasts and lymphocytes,
CC   promoting wound healing, and in enhancing the activity of a therapeutic
CC   agent. The sequences shown in ABR00759-ABR00923 represent the bioactive
CC   peptides of the invention.
XX
SQ   Sequence   23 AA;

  Query Match             63.6%;  Score 42;  DB 24;  Length 23;
  Best Local Similarity   78.6%;  Pred. No. 6.5;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              | ||||| |||| |
Db          2 ALALKALKKALKKL 15
```

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RESULT 43
ABR00780
ID   ABR00780 standard; peptide; 15 AA.
XX
AC   ABR00780;
XX
DT   03-APR-2003  (first entry)
XX
DE   Bioactive synthetic peptide FLAK62 AM.
XX
KW   Antibacterial; fungicide; cytostatic; vulnerary; cancer; cystic fibrosis;
KW   acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
KW   bioactive.
XX
OS   Synthetic.
XX
FH   Key             Location/qualifiers
FT   Modified-site   15
FT                   /note= "C-terminal amide"
XX
PN   WO200279488-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US009534.
XX
PR   28-MAR-2001; 2001US-279505P.
PR   28-MAR-2001; 2001US-0820054.
XX
PA   (HELI ) HELIX BIOMEDIX INC.
XX
PI   Owen DR;
XX
DR   WPI; 2003-221247/21.
XX
PT   New isolated peptide for treating cancer, cystic fibrosis, wounds or
PT   acne, inhibiting growth of microbial cells, or promoting proliferation
PT   of cells, comprises phenylalanine, leucine, alanine or lysine residues
PT
XX
PS   Example 2; Page 6; 134pp; English.
XX
CC   The invention relates to a novel isolated peptide which is 5-23 amino
CC   acids in length, and comprising phenylalanine, leucine, alanine or lysine
CC   residues, or contains at least 50 % of the residues. The peptides of the
CC   invention have antibacterial, fungicide, cytostatic, and vulnerary
CC   activity. The peptides are useful in treating cancer, cystic fibrosis or
CC   acne, inhibiting the growth of microbial cells, promoting the
CC   stimulation and/or proliferation of human fibroblasts and lymphocytes,
CC   promoting wound healing, and in enhancing the activity of a therapeutic
CC   agent. The sequences shown in ABR00759 ABR00923 represent the bioactive
CC   peptides of the invention.
XX
SQ   Sequence   15 AA;

  Query Match             62.1%;  Score 41;  DB 24;  Length 15;
  Best Local Similarity   73.3%;  Pred. No. 6;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              |:  ||| || |||
Db          1 FALAKKALKKAKKAL 15


RESULT 44
ABR00774
ID   ABR00774 standard; peptide; 16 AA.
XX
AC   ABR00774;
XX
DT   03-APR-2003  (first entry)
XX
```

```
DE   Bioactive synthetic peptide FLAK 17 AM.
XX
KW   Antibacterial; fungicide; cytostatic; vulnerary; cancer; cystic fibrosis;
KW   acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
KW   bioactive.
XX
OS   Synthetic.
XX
FH   Key             Location/qualifiers
FT   Modified-site   16
FT                   /note= "C-terminal amide"
XX
PN   WO200279488-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US009534.
XX
PR   28-MAR-2001; 2001US-279505P.
PR   28-MAR-2001; 2001US-0820054.
XX
PA   (HELI ) HELIX BIOMEDIX INC.
XX
PI   Owen DR;
XX
DR   WPI; 2003-221247/21.
XX
PT   New isolated peptide for treating cancer, cystic fibrosis, wounds or
PT   acne, inhibiting growth of microbial cells, or promoting proliferation
PT   of cells, comprises phenylalanine, leucine, alanine or lysine residues
PT
XX
PS   Claim 7; Page 5; 134pp; English.
XX
CC   The invention relates to a novel isolated peptide which is 5-23 amino
CC   acids in length, and comprising phenylalanine, leucine, alanine or lysine
CC   residues, or contains at least 50 % of the residues. The peptides of the
CC   invention have antibacterial, fungicide, cytostatic, and vulnerary
CC   activity. The peptides are useful in treating cancer, cystic fibrosis or
CC   acne, inhibiting the growth of microbial cells, promoting the
CC   stimulation and/or proliferation of human fibroblasts and lymphocytes,
CC   promoting wound healing, and in enhancing the activity of a therapeutic
CC   agent. The sequences shown in ABR00759 ABR00923 represent the bioactive
CC   peptides of the invention.
XX
SQ   Sequence   16 AA;

  Query Match             62.1%;  Score 41;  DB 24;  Length 16;
  Best Local Similarity   76.9%;  Pred. No. 6.4;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              |  :|  ||||| |
Db          1 FALALKKALKALKAL 15


RESULT 45
ABR00919
ID   ABR00919 standard; peptide; 23 AA.
XX
AC   ABR00919;
XX
DT   03-APR-2003  (first entry)
XX
DE   Bioactive synthetic peptide FLAK63AMV.
XX
KW   Antibacterial; fungicide; cytostatic; vulnerary; cancer; cystic fibrosis;
KW   acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
KW   bioactive.
XX
OS   Synthetic.
XX
FH   Key             Location/qualifiers
```

```
FT   Modified-site   23
FT                   /note= "C-terminal amide"
XX
PN   WO200279408-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US09534.
XX
PR   28-MAR-2001; 2001US-279505P.
PR   28-MAR-2001; 2001US-0820053.
XX
PA   (HELI-) HELIX BIOMEDIX INC.
XX
PI   Owen DR;
XX
DR   WPI; 2003-221247/21.
XX
PT   New isolated peptide for treating cancer, cystic fibrosis, wounds or
PT   acne, inhibiting growth of microbial cells, or promoting proliferation
PT   of cells, comprises phenylalanine, leucine, alanine or lysine residues
PT   -
XX
PS   Example 2; Page 9; 133pp; English.
XX
CC   The invention relates to a novel isolated peptide which is 5-23 amino
CC   acids in length, and comprising phenylalanine, leucine, alanine or lysine
CC   residues, or contains at least 50 % of the residues. The peptides of the
CC   invention have antibacterial, fungicide, cytostatic, and vulnerary
CC   activity. The peptides are useful in treating cancer, cystic fibrosis or
CC   acne, inhibiting the growth of microbial cells, promoting the
CC   stimulation and/or proliferation of human fibroblasts and lymphocytes,
CC   promoting wound healing, and in enhancing the activity of a therapeutic
CC   agent. The sequences shown in ABR00759-ABR00923 represent the bioactive
CC   peptides of the invention.
XX
SQ   Sequence   23 AA;

  Query Match             62.1%;  Score 41;  DB 24;  Length 23;
  Best Local Similarity   76.9%;  Pred. No. 9.3;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 KALKALLKALKAL 15
              |||| ||| || |
Db          6 KALKKLLKKLKKL 18


Search completed: August 21, 2003, 08:19:03
Job time : 84 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 21, 2003, 08:08:00 ; Search time 94 Seconds
(without alignments)
41.179 Million cell updates/sec

Title: US-09-820-053A-43
Perfect score: 66
Sequence: 1 FAKALKALLKALKAL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 10083

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	29	43.9	20	2	Q56130	Q56130 salmonella
2	26	39.4	21	2	Q46010	Q46010 clostridium
3	26	39.4	21	2	Q46011	Q46011 clostridium
4	26	39.4	25	15	Q9d...28	Q9d...28 human immun
5	26	39.4	25	15	Q99bq6	Q99bq6 human immun
6	26	39.4	25	15	Q9...17	Q9...17 human immun
7	25	37.9	18	1	Q9UWL7	Q9UWL7 methanosarc
8	24	36.4	11	2	P77404	P77404 escherichia
9	24	36.4	11	2	P95518	P95518 pasteurella
10	24	36.4	19	2	Q9r5j9	Q9r5j9 acinetobact
11	24	36.4	20	13	P82876	P82876 rana clamit
12	24	36.4	24	5	Q9N685	Q9N685 strongyloce
13	23	34.8	15	13	P83333	P83333 oncorhynchu
14	23	34.8	17	8	Q9G468	Q9G468 brassica ju
15	23	34.8	19	4	Q99711	Q99711 homo sapien
16	23	34.8	22	12	Q87029	Q87029 pseudorabie
17	23	34.8	25	15	Q99BE4	Q99BE4 human immun
18	23	34.8	25	15	Q99BS6	Q99BS6 human immun
19	23	34.8	25	15	Q99BN8	Q99BN8 human immun
20	22	33.3	11	2	Q8GLI9	Q8GLI9 bordetella
21	22	33.3	15	2	Q9R4F0	Q9R4F0 desulfovib
22	22	33.3	15	8	Q912Q2	Q912Q2 chlamydia m
23	22	33.3	17	4	Q14001	Q14001 homo sapien
24	22	33.3	18	2	Q92J42	Q92J42 chlamydia p
25	22	33.3	18	2	Q9R4P1	Q9R4P1 brevibacter
26	22	33.3	18	10	Q9SB18	Q9SB18 solanum tub
27	22	33.3	19	4	Q9UK05	Q9UK05 homo sapien
28	22	33.3	20	6	Q9BE76	Q9BE76 sus scrofa
29	22	33.3	20	13	P82877	P82877 rana clamit
30	22	33.3	21	4	Q8N550	Q8N550 homo sapien
31	22	33.3	23	12	Q87082	Q87082 pseud rabie
32	22	33.3	23	12	Q87...1	Q87...1 pseudorabie
33	22	33.3	23	12	Q87083	Q87083 pseudorabie
34	22	33.3	24	4	Q8WYI9	Q8WYI9 homo sapien
35	22	33.3	25	8	Q9T213	Q9T213 brassica n
36	22	33.3	25	10	Q40972	Q40972 pisum sativ
37	22	33.3	25	15	Q99BP7	Q99BP7 human immun
38	22	33.3	25	15	Q99BN0	Q99BN0 human immun
39	22	33.3	25	15	Q99BL1	Q99BL1 human immun
40	22	33.3	25	15	Q99BQ0	Q99BQ0 human immun
41	22	33.3	25	15	Q99BT5	Q99BT5 human immun
42	22	33.3	25	15	Q99BL9	Q99BL9 human immun
43	22	33.3	25	15	Q9W8V6	Q9W8V6 human immun
44	22	33.3	25	15	Q99BI1	Q99BI1 human immun
45	22	33.3	25	15	Q99BM8	Q99BM8 human immun

ALIGNMENTS

RESULT 1
Q56130
ID Q56130 PRELIMINARY; PRT; 20 AA.
AC Q56130;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Typhimurium rpoB RNA polymerase beta subunit (Fragment).
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RA Svetlov E.D., Lisitsyn N.A., Gorlov S.G., Monastyrskaya G.S.;
RT "Nucleotide Sequence of the rpoB Gene of Salmonella typhimurium.
RT Coding for the Beta Subunit of RNA Polymerase.";
RL Dokl. Biochem. 287:232-236(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA Svetlov E.D., Lisitsyn N.A., Gorlov S.G., Monastyrskaya G.S.;
RT "Nucleotide sequence of the rpoB gene of Salmonella typhimurium coding
RT for the beta-subunit of RNA polymerase.";
RL Dokl. Biochem. 287:62-65(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87072707; PubMed=3656723;
RA Lisitsyn N.A., Monastyrskaya G.S., Svetlov E.D.;
RT "Genes coding for RNA polymerase beta subunit in bacteria.";
RL Eur. J. Biochem. 177:363-369(1988).
DR EMBL; X04642; CAA28303.1; -.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2270 MW; 624C42B9B6B675A CRC64;

Query Match 43.9%; Score 29; DB 2; Length 20;
Best Local Similarity 70.0%; Pred. No. 5.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Q1 F KALKALLKALKAL 14

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                  :| ||| |||
Db          1 MKHLLKPLKA 10


RESULT 2
Q46010
ID   Q46010       PRELIMINARY;       PRT;    21 AA.
AC   Q46010;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Orf protein (Fragment).
GN   ORF.
OS   Clostridium cochlearium.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1494;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DSM 1285;
RX   MEDLINE=94283856; PubMed=8013871;
RA   Zelder O., Beatrix B., Buckel W.;
RT   "Cloning, sequencing and expression in Escherichia coli of the gene
RT   encoding component S of the coenzyme B12-dependent glutamate mutase
RT   from Clostridium cochlearium.";
RL   FEMS Microbiol. Lett. 118:15-21(1994).
DR   EMBL; X75890; CAA53483.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   21 AA;  2347 MW;  82EB2CA4CB66D2EF CRC64;

  Query Match             39.4%;  Score 26;  DB 2;  Length 21;
  Best Local Similarity   58.8%;  Pred. No. 1.7e+03;
  Matches    7;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 KALKALEKALKAL 15
              |||:: |  :: |
Db          8 KALESKELEVKYL 20


RESULT 3
Q46011
ID   Q46011       PRELIMINARY;       PRT;    21 AA.
AC   Q46011;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   GlmS, glmE and glmL genes (Fragment).
OS   Clostridium cochlearium.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1494;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DSM 1285;
RX   MEDLINE=96094816; PubMed=7880251;
RA   Zelder O., Beatrix B., Leutbecher U., Buckel W.;
RT   "Characterization of the coenzyme B12-dependent glutamate mutase from
RT   Clostridium cochlearium produced in Escherichia coli.";
RL   Eur. J. Biochem. 226:577-585(1994).
DR   EMBL; X80997; CAA56920.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   21 AA;  2379 MW;  82EB2CA41A67C2EF CRC64;

  Query Match             39.4%;  Score 26;  DB 2;  Length 21;
  Best Local Similarity   58.8%;  Pred. No. 1.7e+03;
  Matches    7;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 KALKALEKALKAL 15
              |||:: |  :: |
Db          8 KALESKELEVKYL 20


RESULT 4
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Q9DH28
ID   Q9DH28       PRELIMINARY;       PRT;    21 AA.
AC   Q9DH28;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Rev protein (Fragment).
GN   REV.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mi0012;
RX   MEDLINE=21002578; PubMed=11119006;
RA   Motomura K., Kusagawa S., Kato K., Nakano K., Iwa...
RA   Thwe M., ... K.Y., Lwin S., Kyaw ..., Zaw M., Naka... Y., Tanaka T.;
RT   "Emergence of new forms of human immunodeficiency virus type 1
RT   intersubtype recombinants in central myanmar.";
RL   AIDS Res. Hum. Retroviruses 16:1841-1844(2000).
DR   EMBL; AB034602; BAB19227.1; -.
DR   InterPro; IPR000625; REV protein.
DR   Pfam; PF00424; REV; 1.
FT   NON_TER       21      21
SQ   SEQUENCE   21 AA;  2749 MW;  4E9C43F8AC43E248 CRC64;

  Query Match             39.4%;  Score 26;  DB 2;  Length 21;
  Best Local Similarity   50.0%;  Pred. No. ...e+03;
  Matches    5;  Conservative    4;  Mismatches    3;  Indels    ...;  Gaps    ...;

Qy          6 KALLKALKALKAL 19
              :|||:::: :
Db          1 EALLKAVKVLL 10


RESULT 5
Q9YBQ6
ID   Q9YBQ6       PRELIMINARY;       PRT;    21 AA.
AC   Q9YBQ6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Rev protein (Fragment).
GN   REV.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IV0006.96;
RX   MEDLINE=21422628; PubMed=11429118;
RA   Scriba T.J., Treurnicht F.K., Zeier M., Esser...
RA   van Rensburg E.J.;
RT   "Characterization and phylogenetic analysis ... ... ... ...
RT   subtype C accessory genes.";
RL   AIDS Res. Hum. Retroviruses 17:777-781(2001).
DR   EMBL; AF327...; AAE06...; -.
DR   InterPro; IPR000625; REV protein.
DR   Pfam; PF00424; REV; 1.
FT   NON_TER       21      21
SQ   SEQUENCE   21 AA;  2721 MW;  9CAF09E3BAE...  CRC64;

  Query Match             39.4%;  Score 26;  DB 2;  Length 21;
  Best Local Similarity   50.0%;  Pred. No. ...e+03;
  Matches    5;  Conservative    4;  Mismatches    3;  Indels    ...;  Gaps    ...;

Qy          6 KALLKALKALKAL 19
              :|||:::: :
Db          1 EALLQAVKVLL 10


RESULT 6
Q9DH17
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ID   Q9DUL7      PRELIMINARY;      PRT;    25 AA.
AC   Q9DUL7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Rev protein (Fragment).
GN   REV.
OS   Human immunodeficiency virus 1
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN m10018;
RX   MEDLINE=21002574; PubMed=11118069;
RA   Motomura F., Fukasawa S., Kato K., Nishimi K., Lwin H.H., Tun K.K.,
RA   Thwe M., Oo K.Y., Lwin S., Kyaw O., Zaw M., Nagai Y., Takebe Y.;
RT   "Emergence of new forms of human immunodeficiency virus type 1
RT   intersubtype recombinants in central myanmar.";
RL   AIDS Res. Hum. Retroviruses 16:1831-1843(2000).
DR   EMBL; AB043904; BAB19238.1; -.
DR   InterPro; IPR000625; REV_protein.
DR   Pfam; PF00424; REV; 1.
FT   NON_TER      25      25
SQ   SEQUENCE   25 AA;  2735 MW;  4E933F58AC4F224B CRC64;

  Query Match             39.4%;  Score 26;  DB 15;  Length 25;
  Best Local Similarity   50.0%;  Pred. No. 2.1e+03;
  Matches    5;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 KALLKALKAL 15
              :|||||:: :
Db         10 EALLKAVRII 19


RESULT 7
Q9UWL7
ID   Q9UWL7      PRELIMINARY;      PRT;    18 AA.
AC   Q9UWL7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   METHYLCOBALAMIN: coenzyme M methyltransferase isoenzyme II (Fragment).
OS   Methanosarcina barkeri.
OC   Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC   Methanosarcinaceae; Methanosarcina.
OX   NCBI_TaxID=2208;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93356596; PubMed=8352643;
RA   Yeliseev A., Gartner P., Harms U., Linder D., Thauer R.K.;
RT   "Function of methylcobalamin: coenzyme M methyltransferase isoenzyme
RT   II in Methanosarcina barkeri.";
RL   Arch. Microbiol. 159:530-536(1993).
SQ   SEQUENCE   18 AA;  1916 MW;  18D4422F64822B75 CRC64;

  Query Match             37.9%;  Score 25;  DB 1;  Length 18;
  Best Local Similarity   66.7%;  Pred. No. 2.2e+03;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 LKALLKALK 13
              || || ||:
Db          5 LKTLLAALE 13


RESULT 8
P77404
ID   P77404      PRELIMINARY;      PRT;    11 AA.
AC   P77404;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   DNA sequence downstream of the ECOPRRI HSD locus (Fragment).
GN   HSDR.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97206151; PubMed=9157244;
RA   Tyndall C., Lohbauer B., Sandmeier U., Kulik E., Bickle T.A.;
RT   "The 5'-terminal half of the restriction subunit (HsdR) of the
RT   high homology to the phage P1 genome: implications for the origin
RT   and spread of DNA restriction systems.";
RL   Mol. Microbiol. 23:729-736(1997).
DR   EMBL; X98145; CAA66840.1; -.
DR   EMBL; X98144; CAA66839.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   11 AA;  1259 MW;  714AB0F9254B7A54 CRC64;

  Query Match             36.4%;  Score 24;  DB 2;  Length 11;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+03;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 LKALKA 14
              |||:||
Db          5 LKSLKA 11


RESULT 9
P95518
ID   P95518      PRELIMINARY;      PRT;    11 AA.
AC   P95518;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Ribosomal protein RpsA (Fragment).
GN   RPSA.
OS   Pasteurella haemolytica.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC   Pasteurellaceae; Mannheimia.
OX   NCBI_TaxID=75985;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN PH101;
RX   MEDLINE=97134347; PubMed=9013038;
RA   Highlander S.K., Garza O., Brown R.J., Kuby S., Oppedisano A.B.;
RT   "Isolation and characterization of the integration host factor genes
RT   of Pasteurella haemolytica.";
RL   FEMS Microbiol. Lett. 146:183-188(1997).
DR   EMBL; U56139; AAC44845.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   11 AA;  1168 MW;  7A4BFD38D3396DB8 CRC64;

  Query Match             36.4%;  Score 24;  DB 2;  Length 11;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+03;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FAKALKA 7
              ||:| ||
Db          2 FAEAPEA 8


RESULT 10
Q9R519
ID   Q9R519      PRELIMINARY;      PRT;    19 AA.
AC   Q9R519;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   L-2,4-diaminobutyrate decarboxylase (Fragment).
OS   Acinetobacter calcoaceticus.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Moraxellaceae; Acinetobacter.
OX   NCBI_TaxID=471;
RN   [1]
```

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PF   SEQUENCE.
RX   MEDLINE 92481494; PubMed=1512577;
RA   Yamamoto S., Tsuzaki Y., Tougou K., Shinoda S.;
RT   "Purification and characterization of L 2,4-diaminobutyrate
RT   decarboxylase from Acinetobacter calcoaceticus.";
RL   J. Gen. Microbiol. 138:1461 1465(1992).
SQ   SEQUENCE   19 AA;  2185 MW;  50F49796DD1B9912 CRC64;

  Query Match             36.4%;  Score 24;  DB 2;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 3.5e+03;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FAKALKALL 9
              :|:  ||||
Db          3 FAEHRKALL 11


RESULT 11
P82876
ID   P82876       PRELIMINARY;      PRT;    20 AA.
AC   P82876;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Ranalexin-1CA.
OS   Rana clamitans (green frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=145282;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin;
RX   MEDLINE 20283865; PubMed=10822101;
RA   Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;
RT   "Purification and characterization of antimicrobial peptides from the
RT   skin of the North American green frog Rana clamitans.";
RL   Peptides 21:469-476(2000).
CC   -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC       S.AUREUS AND GRAM-NEGATIVE BACTERIUM E.COLI. HAS ACTIVITY AGAINST
CC       C.ALBICANS.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC   -!- MASS SPECTROMETRY: MW=2187.0; MW_ERR=0.02; METHOD=ELECTROSPRAY.
CC   -!- SIMILARITY: BELONGS TO A NOVEL FAMILY OF PREVIOUSLY CHARACTERIZED
CC       FAMILY.
KW   Antibiotic; Fungicide.
FT   NON_TER      14      20
SQ   SEQUENCE   20 AA;  2112 MW;  2A708028F7B826B7 CRC64;

  Query Match             36.4%;  Score 24;  DB 13;  Length 20;
  Best Local Similarity   54.5%;  Pred. No. 3.5e+03;
  Matches    6;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 LKALLKALKAL 15
              |  |:||  ||
Db          2 LGGLMKAFPAL 12


RESULT 12
Q9N685
ID   Q9N685       PRELIMINARY;      PRT;    24 AA.
AC   Q9N685;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Scavenger receptor cysteine-rich protein (Fragment).
OS   Strongylocentrotus purpuratus (Purple sea urchin).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC   Strongylocentrotus.
OX   NCBI_TaxID=7668;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SRC861.4, and SRC861.1;
RA   Pancer Z.;
RT   "Dynamic Repertoires of Putative Immune Cell Receptors in the Sea
RT   Urchin.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF228674; AAF78972.1; -.
DR   EMBL; AF228673; AAF78971.1; -.
KW   Receptor.
FT   NON_TER      24      24
SQ   SEQUENCE   24 AA;  2289 MW;  B9A719A2??B0A??? CRC64;

  Query Match             36.4%;  Score 24;  DB ?;  Length 24;
  Best Local Similarity   70.0%;  Pred. No. 4.?e+03;
  Matches    7;  Conservative    0;  Mismatches    ??;  Indels    ??;  Gaps    ??;

Qy          5 LKALLKALKA 14
              | |||| || |
Db          6 LSALLVALVA 15


RESULT 13
P83333
ID   P83333       PRELIMINARY;      PRT;    15 AA.
AC   P83333;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Lysozyme C III (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C
DE   (Fragment).
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salmoninae;
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE, CATALYTIC ACTIVITY, AND MASS SPECTROMETRY.
RC   TISSUE=Skin mucus;
RA   Fernandes J.M.O., Kemp G.D., Smith V.J.;
RT   "Characterisation of two muramidases from skin mucus of rainbow
RT   trout.";
RL   Submitted (APR-2002) to the SWISS-PROT data bank.
CC   -!- FUNCTION: LYSOZYMES HAVE BACTERIOLYTIC AND NON-ENZYMIC HOST-
CC       DEFENCE ANTIMICROBIAL ACTIVITIES. THEY ARE ABUNDANT IN MANY
CC       MAMMALIAN SECRETIONS AND BODY FLUIDS.
CC   -!- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-LINKAGES BETWEEN N-
CC       ACETYL-D-GLUCOSAMINE AND N-ACETYLMURAMIC ACID IN BOTH
CC       HETEROPOLYMERS OF THE PEPTIDOGLYCAN CELL WALL.
CC   -!- MASS SPECTROMETRY: MW=14247; METHOD=MALDI.
CC   -!- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
DR   InterPro; IPR001916; Glyco_hydro_22;
DR   PROSITE; PS00128; LACTALBUMIN_LYSOZYME; FALSE;
KW   Hydrolase; Glycosidase; Bacteriolytic enzyme.
FT   NON_TER      15      15
SQ   SEQUENCE   15 AA;  1665 MW;  4FEL1DEL7A0CBF7 CRC64;

  Query Match             34.8%;  Score 23;  DB ?;  Length ?;
  Best Local Similarity   83.3%;  Pred. No. 5.8e+03;
  Matches    5;  Conservative    1;  Mismatches    ??;  Indels    ??;  Gaps    ??;

Qy          2 AKALKA 7
              :||||:
Db          9 AKALKA 14


RESULT 14
Q9G468
ID   Q9G468       PRELIMINARY;      PRT;    17 AA.
AC   Q9G468;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Hypothetical 2.0 kDa protein.
OS   Brassica juncea (Leaf mustard) (Indian mustard).
OC   Mitochondrion.
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OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Brassica.
OX   NCBI_TaxID=3707;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN cv. Zhetong no. 1;
RA   Chen X.J., Zhang Y.Z., Chen Z.J., Jin Y.;
RT   "A specific mtDNA fragment related to cytoplasmic male sterility in
RT   tuber mustard.";
RL   Submitted (AUG 2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF298549; AAG39440.1; -.
KW   Hypothetical protein; Mitochondrion.
SQ   SEQUENCE   17 AA;  2019 MW;  53697CDBFE69EE26 CRC64;

  Query Match             34.8%;  Score 23;  DB 8;  Length 17;
  Best Local Similarity   55.6%;  Pred. No. 4.3e+03;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 KALKALLKA 11
              | || |:|:
Db          8 KQLKMLVKS 16


RESULT 15
Q99711
ID   Q99711       PRELIMINARY;      PRT;    19 AA.
AC   Q99711;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Gamma-glutamylcysteine synthetase light subunit (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98278974; PubMed=9614065;
RA   Moinova H.R., Mulcahy R.T.;
RT   "An electrophile responsive element (EpRE) regulates beta-
RT   naphthoflavone induction of the human gamma-glutamylcysteine
RT   synthetase regulatory subunit gene. Constitutive expression is
RT   mediated by an adjacent ap-1 site.";
RL   J. Biol. Chem. 273:14683-14689(1998).
DR   EMBL; U72210; AAC24417.1; -.
FT   NON_TER      19      19
SQ   SEQUENCE   19 AA;  1993 MW;  5E379EA26886D15C CRC64;

  Query Match             34.8%;  Score 23;  DB 4;  Length 19;
  Best Local Similarity   62.5%;  Pred. No. 4.8e+03;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALKALL 9
              ::: ||||
Db          5 SRAAKALL 12


RESULT 16
Q87078
ID   Q87078       PRELIMINARY;      PRT;    23 AA.
AC   Q87078;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Glycoprotein C precursor (Fragment).
GN   GC.
OS   Pseudorabies virus.
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Varicellovirus.
OX   NCBI_TaxID=10345;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Becker;
RX   MEDLINE 96070924; PubMed 7499261;
RA   Ryan P., Edwards C.O.;
RT   "Systematic introduction of proline in a eukaryotic signal sequence
RT   suggests asymmetry within the hydrophobic core.";
RL   J. Biol. Chem. 270:27876-27879(1995).
DR   EMBL; U29121; AAC54531.1; -.
KW   Signal.
FT   SIGNAL       1      22       POTENTIAL.
FT   NON_TER     23      23
SQ   SEQUENCE   23 AA;  2229 MW;  B2112B1D21407473 CRC64;

  Query Match             34.8%;  Score 23;  DB 12;  Length 23;
  Best Local Similarity   62.5%;  Pred. No. 5.8e+03;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALKALL 9
              |:|: |||
Db          5 ARAMPALL 12


RESULT 17
Q99BR3
ID   Q99BR3       PRELIMINARY;      PRT;    25 AA.
AC   Q99BR3;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Rev protein (Fragment).
GN   REV.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN TV005-81;
RX   MEDLINE 21322026; PubMed=11429118;
RA   Soriba T.J., Iroanwicht F.K., Zeier M., Engelbrecht S.,
RA   Van Rensburg E.J.;
RT   "Characterization and phylogenetic analysis of South African HIV-1
RT   subtype C accessory genes.";
RL   AIDS Res. Hum. Retroviruses 17:777-781(2001).
DR   EMBL; AF325747; AAK09125.1; -.
DR   InterPro; IPR000625; REV_protein.
DR   Pfam; PF00424; REV; 1.
FT   NON_TER      25      25
SQ   SEQUENCE   25 AA;  2727 MW;  D2933E1439EF220A CRC64;

  Query Match             34.8%;  Score 23;  DB 15;  Length 25;
  Best Local Similarity   40.0%;  Pred. No. 6.9e+03;
  Matches    4;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 KALLKALKAL 15
              :|||:::: :
Db         10 EALLQAVRTI 19


RESULT 18
Q99BS6
ID   Q99BS6       PRELIMINARY;      PRT;    25 AA.
AC   Q99BS6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Rev protein (Fragment).
GN   REV.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN TV004-45;
RX   MEDLINE 21422026; PubMed 11429118;
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RA   Scriba T.J., Tournicht F.K., Zeier M., Engelbrecht S.,
RA   van Rensburg E.J.;
RT   "Characterization and phylogenetic analysis of South African HIV-1
RT   subtype C accessory genes.";
RL   AIDS Res. Hum. Retroviruses 17:775-781(2001).
DR   EMBL; AF325744; AAK09110.1;  -.
DR   InterPro; IPR000625; REV_protein.
DR   Pfam; PF00424; REV; 1.
FT   NON_TER      25     25
SQ   SEQUENCE   25 AA;  2723 MW;  D7933F445E4F225A CRC64;

  Query Match             34.8%;  Score 23;  DB 15;  Length 25;
  Best Local Similarity   40.0%;  Pred. No. 6.6e+03;
  Matches    4;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 KALLKALKAL 15
              :|||:|:: :
Db         10 EALLQAVRTI 19


RESULT 19
Q99BN8
ID   Q99BN8       PRELIMINARY;       PRT;    25 AA.
AC   Q99BN8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Rev protein (Fragment).
GN   REV.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN IV012 4;
RX   MEDLINE 21322026; PubMed 11429119;
RA   Scriba T.J., Tournicht F.K., Zeier M., Engelbrecht S.,
RA   van Rensburg E.J.;
RT   "Characterization and phylogenetic analysis of South African HIV-1
RT   subtype C accessory genes.";
RL   AIDS Res. Hum. Retroviruses 17:775-781(2001).
DR   EMBL; AF325754; AAK09160.1;  -.
DR   InterPro; IPR000625; REV_protein.
DR   Pfam; PF00424; REV; 1.
FT   NON_TER      25     25
SQ   SEQUENCE   25 AA;  2750 MW;  D786E5745E4F225A CRC64;

  Query Match             34.8%;  Score 23;  DB 15;  Length 25;
  Best Local Similarity   40.0%;  Pred. No. 6.6e+03;
  Matches    4;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 KALLKALKAL 15
              :|||:|:: :
Db         10 EALLQAVRTI 19


RESULT 20
Q8GLI9
ID   Q8GLI9       PRELIMINARY;       PRT;    11 AA.
AC   Q8GLI9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   PF 50 protein (Fragment).
GN   PF 50.
OS   Borrelia burgdorferi (Lyme disease spirochete).
OG   Plasmid qrump cp32-11.
OC   Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX   NCBI_TaxID=139;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN SH-2-82;
RA   Stevenson B., Miller J.C.;
RT   "Comparative analyses of Borrelia burgdorferi cp32 circular
RT   prophages: conservation amidst diversity.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY142706; AAN12880.1;  -.
KW   Plasmid.
FT   NON_TER      1      1
SQ   SEQUENCE   11 AA;  1366 MW;  4E44CD5C6C4A5C76 CRC64;

  Query Match             33.4%;  Score 22;  DB 2;  Length 11;
  Best Local Similarity   55.6%;  Pred. No. 4.2e+03;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 LKALLKALKAL 15
              :|:|:||:|:
Db          2 IKWLLKNLKIL 12


RESULT 21
Q9R4F0
ID   Q9R4F0       PRELIMINARY;       PRT;    15 AA.
AC   Q9R4F0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Formate dehydrogenase gamma subunit (Fragment)
OS   Desulfovibrio vulgaris.
OC   Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC   Desulfovibrionaceae; Desulfovibrio.
OX   NCBI_TaxID=881;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE 96037504; PubMed 8566569;
RA   Sebban C., Blanchard L., Bruschi M., Guerlesquin F.;
RT   "Purification and characterization of the 3 heme c containing
RT   Desulfovibrio vulgaris Hildenborough.";
RL   FEMS Microbiol. Lett. 143:141-145(1996).
FT   NON_TER      1      1
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1591 MW;  F3A06AEC15C27C9 CRC64;

  Query Match             33.4%;  Score 22;  DB 2;  Length 15;
  Best Local Similarity   55.6%;  Pred. No. 5.5e+03;
  Matches    5;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 AKALKALKALKAL 14
              : :|| |||:|:
Db          1 ADAAKAPKKAIE 12


RESULT 22
Q9TZQ2
ID   Q9TZQ2       PRELIMINARY;       PRT;    15 AA.
AC   Q9TZQ2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   11 kD respiratory protein (Fragment).
OS   Chlamydomonas reinhardtii.
OG   Mitochondrion.
OC   Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC   Chlamydomonadaceae; Chlamydomonas.
OX   NCBI_TaxID=3055;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE 95079249; PubMed 7826432;
RA   Atteia A.;
RT   "Identification of mitochondrial respiratory [illegible] in the
RT   alga Chlamydomonas reinhardtii.";
RL   C. R. Acad. Sci., III, Sci. Vie 317:1143-1149(1994).
SQ   SEQUENCE   15 AA;  1689 MW;  B3EB7A9417215A4E CRC64;

  Query Match             33.4%;  Score 22;  DB 2;  Length 15;
  Best Local Similarity   66.7%;  Pred. No. 5.5e+03;
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  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AKALKALLK 10
              |||| | |
Db          4 AKALDELRK 12


RESULT 23
Q14001
ID   Q14001       PRELIMINARY;      PRT;    17 AA.
AC   Q14001;
DT   02-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Cyclic nucleotide phosphodiesterase (Fragment).
GN   CGIPDE1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97079687; PubMed=8921398;
RA   Loebbert R.W., Winterpacht A., Seipel B., Zabel B.U.;
RT   "Molecular cloning and chromosomal assignment of the human homologue
RT   of the rat cGMP-inhibited phosphodiesterase 3 (PDE3A) A gene involved
RT   in fat metabolism located at 11p15.1.";
RL   Genomics 37:211-218(1996).
DR   EMBL; X99522; CAA67776.1; -.
FT   NON_TER      17      17
SQ   SEQUENCE   17 AA;  2057 MW;  69D117C4FAE11540 CRC64;

  Query Match             33.3%;  Score 22;  DB 4;  Length 17;
  Best Local Similarity   57.1%;  Pred. No. 6.3e+03;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AKALKAL 8
              |||:::|
Db          8 AKAMRSL 14


RESULT 24
Q9ZG42
ID   Q9ZG42       PRELIMINARY;      PRT;    18 AA.
AC   Q9ZG42;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   Proline transport protein (Fragment).
OS   Chlamydia trachomatis.
OC   Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX   NCBI_TaxID=813;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=L2 434B;
RA   Wang L., Stoenburg S.D., Zheng Y., Larsen S.H.;
RT   "Gene identification of Chlamydia trachomatis by random DNA
RT   sequencing.";
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF087825; AAD04100.1; -.
FT   NON_TER      1       1
FT   NON_TER     18      18
SQ   SEQUENCE   18 AA;  2236 MW;  5504A82ED42CC261 CRC64;

  Query Match             33.3%;  Score 22;  DB 2;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.6e+03;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FAKALK 6
              | |||:|
Db         10 FYEALK 15


RESULT 25
Q9R4P1
ID   Q9R4P1       PRELIMINARY;      PRT;    18 AA.
AC   Q9R4P1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   Ribosomal protein S21 (Fragment).
OS   Brevundimonas vesicularis (Pseudomonas vesicularis).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC   Caulobacteraceae; Brevundimonas.
OX   NCBI_TaxID=41276;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=96244309; PubMed=7727274;
RA   Ochi K.;
RT   "Comparative ribosomal protein sequence analyses. I. [illegible]
RT   defined genus, Pseudomonas, and its relatives.";
RL   Int. J. Syst. Bacteriol. 45:268-273(1995).
SQ   SEQUENCE   18 AA;  2071 MW;  C7C7A475124F1E5E CRC64;

  Query Match             33.3%;  Score 22;  DB 2;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 6.6e+03;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 KALKAL 8
              :|||||
Db         12 QALKAL 17


RESULT 26
Q9SB18
ID   Q9SB18       PRELIMINARY;      PRT;    18 AA.
AC   Q9SB18;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Potato patatin (Fragment).
OS   Solanum tuberosum (Potato).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX   NCBI_TaxID=4113;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Twell D., Coms G.;
RT   "The 5' flanking DNA of a patatin gene directs tuber specific
RT   expression of a chimaeric gene in potato.";
RL   Plant Mol. Biol. 9:345-375(1987).
DR   EMBL; M17640; AAA33818.1; -.
FT   NON_TER      1       1
SQ   SEQUENCE   18 AA;  2109 MW;  [illegible] CRC64;

  Query Match             55.5%;  Score 22;  DB 10;  Length 18;
  Best Local Similarity   50.0%;  Pred. No. 6.6e+03;
  Matches    8;  Conservative    2;  Mismatches    4;  Indels    2;  Gaps    2;

Qy          1 FAKAL KALLKALKA 14
              |:|:|  :  |:|:|
Db          1 FAKLLSLRKKLPANKA 16


RESULT 27
Q9UKU5
ID   Q9UKU5       PRELIMINARY;      PRT;    18 AA.
AC   Q9UKU5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   Voltage-gated sodium channel NaN (Fragment).
GN   SCN11A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99375324; PubMed=10444332;
RA   Dib-Hajj S.D., Tyrrell L., Escayg A., Wood P.M., Meisler M.H.,
RA   Waxman S.G.;
RT   "Coding sequence, genomic organization, and conserved chromosomal
RT   localization of the mouse gene Scn11a encoding the sodium channel
RT   NaN.";
RL   Genomics 59:309-318(1999).
DR   EMBL; AF126739; AAD53407.1; -.
KW   Ionic channel.
FT   NON_TER       1      1
FT   NON_TER      19     19
SQ   SEQUENCE   19 AA;  2174 MW;  FB014A2387914074 CRC64;

  Query Match             33.3%;  Score 22;  DB 4;  Length 19;
  Best Local Similarity   50.0%;  Pred. No. 7e+03;
  Matches    4;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 LLKALKAL 15
              : :|||:
Db          8 VFRALKAI 15


RESULT 28
Q9BEC6
ID   Q9BEC6       PRELIMINARY;       PRT;    20 AA.
AC   Q9BEC6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Peroxisomal membrane protein 1 (Fragment).
GN   ABCD3.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Pietrain;
RA   Stratil A., Knoblochova S., Peelman L.J., Reiner G., Musilova P.,
RA   Van Poucke M., Rubes J., Geldermann H.;
RT   "FISH, kB and linkage assignment of the porcine ABCD2 (PXMP1) gene 1:
RT   the distal end of chromosome 4q.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ309827; CAC32854.1; -.
FT   NON_TER       1      1
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2215 MW;  A97F37E52C8D5DE8 CRC64;

  Query Match             33.3%;  Score 22;  DB 6;  Length 20;
  Best Local Similarity   33.3%;  Pred. No. 7.4e+03;
  Matches    5;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              |   :  |:: ||| |
Db          3 FTARIFELMQVLKDL 17


RESULT 29
P82877
ID   P82877       PRELIMINARY;       PRT;    20 AA.
AC   P82877;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Ranaloxin-1CB.
OS   Rana clamitans (green frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=145282;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin;
RX   MEDLINE=20283865; PubMed=10822161;
RA   Halverson K., Basir Y.J., Kloczewiak E.C., Conlon J.M.;
RT   "Purification and characterization of antimicrobial peptides from the
RT   skin of the North American green frog Rana clamitans.";
RL   Peptides 21:469-476(2000).
CC   -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC       S.AUREUS AND GRAM-NEGATIVE BACTERIUM E.COLI. HAS ACTIVITY AGAINST
CC       C.ALBICANS (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- MASS SPECTROMETRY: MW=2109.0; METHOD=ELECTROSPRAY.
CC   -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN FAMILY.
CC       FAMILY.
KW   Antibiotic; Fungicide.
FT   DISULFID     14     20
SQ   SEQUENCE   20 AA;  2112 MW;  2821B0AF7D0CC5C7 CRC64;

  Query Match             33.3%;  Score 22;  DB 14;  Length 20;
  Best Local Similarity   45.5%;  Pred. No. 7.4e+03;
  Matches    5;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          6 LKALLKALKAL 16
              :  |:||  |:
Db          2 LGGLMKAFPAI 12


RESULT 30
Q8N550
ID   Q8N550       PRELIMINARY;       PRT;    13 AA.
AC   Q8N550;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg E.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032793; AAH32793.1; -.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   21 AA;  2265 MW;  0E2021FA21C7EE15 CRC64;

  Query Match             33.3%;  Score 22;  DB 5;  Length 21;
  Best Local Similarity   45.2%;  Pred. No. 7.4e+03;
  Matches    6;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKA 14
              | |:  || | |
Db          2 ASAMNILLLGLLA 14


RESULT 31
Q87082
ID   Q87082       PRELIMINARY;       PRT;    23 AA.
AC   Q87082;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1996 (TrEMBLrel. 08, Last annotation update)
DE   Glycoprotein C precursor (Fragment).
GN   GC.
OS   Pseudorabies virus.
OC   Viruses; dsDNA viruses, no RNA stage; Herpesvirales;
OC   Alphaherpesvirinae; Varicellovirus.
OX   NCBI_TaxID=10345;
RN   [1]
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RP   SEQUENCE FROM N.A.
RC   STRAIN Becker;
RX   MEDLINE 96070924; PubMed-7499261;
RA   Ryan P., Edwards C.C.;
RT   "Systematic introduction of proline in a eukaryotic signal sequence
RT   suggests asymmetry within the hydrophobic core.";
RL   J. Biol. Chem. 270:27876 27879(1995).
DR   EMBL; U29125; AAC54535.1; -.
KW   Signal.
FT   SIGNAL         1      22       POTENTIAL.
FT   NON_TER       23      23
SQ   SEQUENCE   23 AA;  2271 MW;  B7113E0B81406F3F CRC64;

  Query Match             33.3%;  Score 22;  DB 12;  Length 23;
  Best Local Similarity   62.5%;  Pred. No. 8.5e+03;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALKALL 9
              |:|: |||
Db          5 ARAMLALL 12


RESULT 32
Q69391
ID   Q69391      PRELIMINARY;      PRT;    23 AA.
AC   Q69391;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV 1998 (TrEMBLrel. 08, Last annotation update)
DE   Glycoprotein C precursor (Fragment).
GN   GC.
OS   Pseudorabies virus.
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Varicellovirus.
OX   NCBI_TaxID=10345;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Becker;
RX   MEDLINE=95081163; PubMed=7989378;
RA   Tomilo M., Wilkinson E.S., Ryan P.,
RT   "Can a signal sequence become too hydrophobic?";
RL   J. Biol. Chem. 269:32016-32021(1994).
DR   EMBL; L36969; AAA79966.1; -.
KW   Signal.
FT   SIGNAL         1      22       POTENTIAL.
FT   NON_TER       23      23
SQ   SEQUENCE   23 AA;  2289 MW;  B7112B1E8146098F CRC64;

  Query Match             33.3%;  Score 22;  DB 12;  Length 23;
  Best Local Similarity   62.5%;  Pred. No. 8.5e+03;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALKALL 9
              |:|: |||
Db          5 ARAMLALL 12


RESULT 33
Q87083
ID   Q87083      PRELIMINARY;      PRT;    23 AA.
AC   Q87083;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Glycoprotein C precursor (Fragment).
GN   GC.
OS   Pseudorabies virus.
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Varicellovirus.
OX   NCBI_TaxID=10345;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Becker;
RX   MEDLINE-96070924; PubMed-7499261;
RA   Ryan P., Edwards C.C.;
RT   "Systematic introduction of proline in a eukaryotic signal sequence
RT   suggests asymmetry within the hydrophobic core.";
RL   J. Biol. Chem. 270:27876 27879(1995).
DR   EMBL; U29126; AAC54546.1; -.
KW   Signal.
FT   SIGNAL         1      22       POTENTIAL.
FT   NON_TER       23      23
SQ   SEQUENCE   23 AA;  2229 MW;  B70A471E81406F3F CRC64;

  Query Match             33.3%;  Score 22;  DB 12;  Length 23;
  Best Local Similarity   62.5%;  Pred. No. 8.5e+03;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AKALKALL 9
              |:|: |||
Db          5 ARAMLALL 12


RESULT 34
Q8WYB9
ID   Q8WYB9      PRELIMINARY;      PRT;    24 AA.
AC   Q8WYB9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Dystrophin (Fragment).
GN   DMD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 7-24 FROM N.A.
RX   MEDLINE-97107974; PubMed-8950674;
RA   Roest P.A., Bout M., van der Tuijn A.C., Ginjaar I.B., Bakker E.,
RA   Hogervorst F.B., van Ommen G.J., den Dunnen J.T.;
RT   "Splicing mutations in DMD/BMD detected by RT-PCR/PTT: detection of a
RT   19AA insertion in the cysteine-rich domain of dystrophin compatible
RT   with BMD.";
RL   J. Med. Genet. 33:935-939(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Roberts R.G.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   den Dunnen J.T.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF213441; AAL61585.1; -.
FT   NON_TER        1       1
FT   NON_TER       24      24
SQ   SEQUENCE   24 AA;  2868 MW;  9C932A2e4F14e3e2 CRC64;

  Query Match             33.3%;  Score 22;  DB 4;  Length 24;
  Best Local Similarity   54.5%;  Pred. No. 8.8e+03;
  Matches    6;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKAL 12
              |  |: | |||
Db         13 AMKLRRLQKAL 23


RESULT 35
Q9T2I3
ID   Q9T2I3      PRELIMINARY;      PRT;    25 AA.
AC   Q9T2I3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   16.1 kDa photosystem I PSAF protein (Fragment).
OS   Nicotiana sylvestris (Wood tobacco).
```

```
OS   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
OX   NCBI_TaxID=4096;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94105345; PubMed=8278548;
RA   Obokata J., Mikami K., Hayashida N., Nakamura M., Sugiura M.;
RT   "Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH, and
RT   psaL are all present in isoforms in Nicotiana spp.";
RL   Plant Physiol. 102:1259-1267(1993).
DR   InterPro; IPR003666; PSI_PsaF.
DR   Pfam; PF02507; PSI_PsaF; 1.
SQ   SEQUENCE   25 AA;  2844 MW;  2E610BFE1922C79E CRC64;

  Query Match             33.3%;  Score 22;  DB 8;  Length 25;
  Best Local Similarity   50.0%;  Pred. No. 9.2e+03;
  Matches    6;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKAL 12
              |:|  |   | |
Db         14 FAKXEKQXXKKL 25


RESULT 36
Q40972
ID   Q40972       PRELIMINARY;      PRT;    25 AA.
AC   Q40972;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   PM2 (Fragment).
GN   PM2.
OS   Pinus radiata (Monterey pine).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX   NCBI_TaxID=3347;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wang D.Y., Bradshaw R.E., Walter C., Connett M., Fountain D.W.;
RT   "Characterisation of the MADS box gene family in Pinus radiata using
RT   PCR cloning.";
RL   Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC       FACTORS.
DR   EMBL; U48626; AAA93370.1; -.
DR   InterPro; IPR002100; TF_MADSbox.
DR   Pfam; PF00319; SRF-TF; 1.
DR   PROSITE; PS50066; MADS_BOX_2; 1.
KW   DNA-binding; Nuclear protein; Transcription; Transcription regulation.
FT   NON_TER       1       1
FT   NON_TER      25      25
SQ   SEQUENCE   25 AA;  2880 MW;  020F92FBAF0CD5F9 CRC64;

  Query Match             33.3%;  Score 22;  DB 10;  Length 25;
  Best Local Similarity   50.0%;  Pred. No. 9.2e+03;
  Matches    5;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLK 10
              |:|    |||
Db          5 FSKRRNGLLK 14


RESULT 37
Q99BP7
ID   Q99BP7       PRELIMINARY;      PRT;    25 AA.
AC   Q99BP7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Rev protein (Fragment).
GN   REV.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IV008_17;
RX   MEDLINE=21422826; PubMed=11420118;
RA   Seriba L.J., Tremeschi F.K., Zeler M., Eyboulet F.;
RA   van Rensburg E.J.;
RT   "Characterization and phylogenetic analysis of South African HIV-1
RT   subtype C accessory genes.";
RL   AIDS Res. Hum. Retroviruses 17:775-781(2001).
DR   EMBL; AF425756; AAK09170.1; -.
DR   InterPro; IPR000625; REV_protein.
DR   Pfam; PF00424; REV; 1.
FT   NON_TER      25      25
SQ   SEQUENCE   25 AA;  2735 MW;  4E433E445E4E124F CRC64;

  Query Match             33.3%;  Score 22;  DB 2;  Length 25;
  Best Local Similarity   40.0%;  Pred. No. 9.2e+03;
  Matches    4;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 KALLKALKAL 15
              :| |:|:: :
Db         10 EALLQAVRII 19


RESULT 38
Q99BN0
ID   Q99BN0       PRELIMINARY;      PRT;    25 AA.
AC   Q99BN0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Rev protein (Fragment).
GN   REV.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IV013_3;
RX   MEDLINE=21422826; PubMed=11420118;
RA   Seriba L.J., Tremeschi F.K., Zeler M., Eyboulet F.;
RA   van Rensburg E.J.;
RT   "Characterization and phylogenetic analysis of South African HIV-1
RT   subtype C accessory genes.";
RL   AIDS Res. Hum. Retroviruses 17:775-781(2001).
DR   EMBL; AF425756; AAK09170.1; -.
DR   InterPro; IPR000625; REV_protein.
DR   Pfam; PF00424; REV; 1.
FT   NON_TER      25      25
SQ   SEQUENCE   25 AA;  2735 MW;  4E433E445E4E124F CRC64;

  Query Match             33.3%;  Score 22;  DB 2;  Length 25;
  Best Local Similarity   40.0%;  Pred. No. 9.2e+03;
  Matches    4;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 KALLKALKAL 15
              :|| |:|:: :
Db         10 EALLQAVRII 19


RESULT 39
Q99BLI
ID   Q99BLI       PRELIMINARY;      PRT;    25 AA.
AC   Q99BLI;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Rev protein (Fragment).
GN   REV.
```

```
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN TV019-82;
RX   MEDLINE 21322026; PubMed=11429118;
RA   Scriba T.J., Treurnicht F.K., Zeier M., Engelbrecht S.,
RA   van Rensburg E.J.;
RT   "Characterization and phylogenetic analysis of South African HIV-1
RT   subtype C accessory genes.";
RL   AIDS Res. Hum. Retroviruses 17:775-781(2001).
DR   EMBL; AF325762; AAK09200.1; -.
DR   InterPro; IPR000625; REV_protein.
DR   Pfam; PF00424; REV; 1.
FT   NON_TER       25       25
SQ   SEQUENCE   25 AA;  2735 MW;  4E933F445E4F224B CRC64;

  Query Match             33.3%;  Score 22;  DB 15;  Length 25;
  Best Local Similarity   40.0%;  Pred. No. 9.2e+03;
  Matches    4;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           6 KALLKALKAL 15
               :|||:|:: :
Db          10 EALLQAVRII 19


RESULT 40
Q99BQ0
ID   Q99BQ0       PRELIMINARY;       PRT;    25 AA.
AC   Q99BQ0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Rev protein (Fragment).
GN   REV.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN TV008-1;
RX   MEDLINE 21322026; PubMed=11429118;
RA   Scriba T.J., Treurnicht F.K., Zeier M., Engelbrecht S.,
RA   van Rensburg E.J.;
RT   "Characterization and phylogenetic analysis of South African HIV-1
RT   subtype C accessory genes.";
RL   AIDS Res. Hum. Retroviruses 17:775-781(2001).
DR   EMBL; AF325751; AAK09145.1; -.
DR   InterPro; IPR000625; REV_protein.
DR   Pfam; PF00424; REV; 1.
FT   NON_TER       25       25
SQ   SEQUENCE   25 AA;  2735 MW;  4E933F445E4F224B CRC64;

  Query Match             33.3%;  Score 22;  DB 15;  Length 25;
  Best Local Similarity   40.0%;  Pred. No. 9.2e+03;
  Matches    4;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           6 KALLKALKAL 15
               :|||:|:: :
Db          10 EALLQAVRII 19


RESULT 41
Q99BT5
ID   Q99BT5       PRELIMINARY;       PRT;    25 AA.
AC   Q99BT5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Rev protein (Fragment).
GN   REV.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=TV001-2;
RX   MEDLINE 21322026; PubMed=11429118;
RA   Scriba T.J., Treurnicht F.K., Zeier M., Engelbrecht S.,
RA   van Rensburg E.J.;
RT   "Characterization and phylogenetic analysis of South African HIV-1
RT   subtype C accessory genes.";
RL   AIDS Res. Hum. Retroviruses 17:775-781(2001).
DR   EMBL; AF325742; AAK09100.1; -.
DR   InterPro; IPR000625; REV_protein.
DR   Pfam; PF00424; REV; 1.
FT   NON_TER       25       25
SQ   SEQUENCE   25 AA;  2735 MW;  4E933F445E4F224B CRC64;

  Query Match             33.3%;  Score 22;  DB 15;  Length 25;
  Best Local Similarity   40.0%;  Pred. No. 9.2e+03;
  Matches    4;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           6 KALLKALKAL 15
               :|||:|:: :
Db          10 EALLQAVRII 19


RESULT 42
Q99BL9
ID   Q99BL9       PRELIMINARY;       PRT;    25 AA.
AC   Q99BL9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Rev protein (Fragment).
GN   REV.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=TV014-4;
RX   MEDLINE 21322026; PubMed=11429118;
RA   Scriba T.J., Treurnicht F.K., Zeier M., Engelbrecht S.,
RA   van Rensburg E.J.;
RT   "Characterization and phylogenetic analysis of South African HIV-1
RT   subtype C accessory genes.";
RL   AIDS Res. Hum. Retroviruses 17:775-781(2001).
DR   EMBL; AF325759; AAK09185.1; -.
DR   InterPro; IPR000625; REV_protein.
DR   Pfam; PF00424; REV; 1.
FT   NON_TER       25       25
SQ   SEQUENCE   25 AA;  2735 MW;  4E933F445E4F224B CRC64;

  Query Match             33.3%;  Score 22;  DB 15;  Length 25;
  Best Local Similarity   40.0%;  Pred. No. 9.2e+03;
  Matches    4;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           6 KALLKALKAL 15
               :|||:|:: :
Db          10 EALLQAVRII 19


RESULT 43
Q9W8V6
ID   Q9W8V6       PRELIMINARY;       PRT;    25 AA.
AC   Q9W8V6;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   REV protein (Fragment).
GN   REV.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
```

```
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CMR709.55, and CMR709.49;
RX   MEDLINE=99329206; PubMed=10400779;
RA   Takehisa J., Zekeng L., Ido E., Yamaguchi-Kabata Y., Mbanya D.,
RA   Harada Y., Miura T., Kaptue L., Hayami M.;
RT   "Human immunodeficiency virus type 1 intergroup (M/O) recombination in
RT   cameroon.";
RL   J. Virol. 73:6810-6820(1999).
DR   EMBL; AF055782; AAD44399.1; -.
DR   EMBL; AF055741; AAD44392.1; -.
DR   InterPro; IPR000625; REV_protein.
DR   Pfam; PF00424; REV; 1.
FT   NON_TER      25      25
SQ   SEQUENCE   25 AA;  2914 MW;  E8D99C5B1B745610 CRC64;

  Query Match             33.3%;  Score 22;  DB 15;  Length 25;
  Best Local Similarity   71.4%;  Pred. No. 9.2e-04;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 KALLKALKAL 14
              | ||||:
Db         10 KDLLKAI 16


RESULT 44
Q99BII
ID   Q99BII      PRELIMINARY;      PRT;    25 AA.
AC   Q99BII;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Rev protein (Fragment).
GN   REV.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IV002-84;
RX   MEDLINE=21322026; PubMed=11429118;
RA   Seriba I.J., Treurnicht F.K., Zeier M., Engelbrecht S.,
RA   van Rensburg E.J.;
RT   "Characterization and phylogenetic analysis of South African HIV-1
RT   subtype C accessory genes.";
RL   AIDS Res. Hum. Retroviruses 17:775-781(2001).
DR   EMBL; AF325743; AAK09105.1; -.
DR   InterPro; IPR000625; REV_protein.
DR   Pfam; PF00424; REV; 1.
FT   NON_TER      25      25
SQ   SEQUENCE   25 AA;  2762 MW;  4E8C85745E4F224B CRC64;

  Query Match             33.3%;  Score 22;  DB 15;  Length 25;
  Best Local Similarity   40.0%;  Pred. No. 9.2e-03;
  Matches    4;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 KALLKALKAL 15
              :|||:|:: :
Db         10 EALLQAVRII 19


RESULT 45
Q99BM8
ID   Q99BM8      PRELIMINARY;      PRT;    25 AA.
AC   Q99BM8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Rev protein (Fragment).
GN   REV.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IV013-2;
RX   MEDLINE=21322026; PubMed=11429118;
RA   Seriba I.J., Treurnicht F.K., Zeier M., Engelbrecht S.,
RA   van Rensburg E.J.;
RT   "Characterization and phylogenetic analysis of South African HIV-1
RT   subtype C accessory genes.";
RL   AIDS Res. Hum. Retroviruses 17:775-781(2001).
DR   EMBL; AF325757; AAK09117.1; -.
DR   InterPro; IPR000625; REV_protein.
DR   Pfam; PF00424; REV; 1.
FT   NON_TER      25      25
SQ   SEQUENCE   25 AA;  2745 MW;  4E9C84E44E4E124B CRC64;

  Query Match             33.3%;  Score 22;  DB 15;  Length 25;
  Best Local Similarity   40.0%;  Pred. No. 9.2e-03;
  Matches    4;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 KALLKALKAL 15
              :|||:|:: :
Db         10 EALLQAVRII 19


Search completed: August 21, 2003, 08:20:46
Job time : 98 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 21, 2003, 08:14:25 ; Search time 22 Seconds
(without alignments)
30.670 Million cell updates/sec

Title: US-09-820-053A-43
Perfect score: 66
Sequence: 1 FAKALKALLKALKAL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 1617

Minimum DB seq length: 0
Maximum DB seq length: 25

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	39.4	14	1	MCRX_METTM	P58815 methanobact
2	25	37.9	14	1	MAST_VESCR	P01516 vespa crabr
3	25	37.9	14	1	MAST_VESLE	P01514 vespula lew
4	25	37.9	14	1	MAST_VESMA	P04205 vespa manda
5	25	37.9	20	1	PCW6_PACCO	P82428 pachycondyl
6	25	37.9	24	1	BOMN_BOMVA	P01505 bombina var
7	24	36.4	14	1	MAST_VESOR	P17238 vespa orien
8	23	34.8	13	1	CBEP_PAPID	P42718 parapolybia
9	23	34.8	20	1	V101_VACCV	P16714 vaccinia vi
10	22	33.3	13	1	RS19_ASHYP	Q44592 ash yellows
11	22	33.3	21	1	JAP2_PANIA	P83206 rana japoni
12	22	33.3	24	1	PCL1_PACCO	P82421 pachycondyl
13	22	33.3	21	1	PCL2_PACCO	P82422 pachycondyl
14	22	33.3	24	1	PGQ_XENLA	P39080 xenopus lae
15	21	31.8	16	1	ALRX_PSEPU	P17916 pseudomonas
16	21	31.8	25	1	Y194_ARCFU	O30045 archaeoglob
17	20	30.3	17	1	UP36_UPEMI	P82043 uperoleia m
18	20	30.3	18	1	OBP_LYMDI	P34173 lymantria d
19	20	30.3	20	1	JHBP_BOMMO	P81627 bombyx mori
20	20	30.3	20	1	SYR_RAT	P40329 rattus norv
21	20	30.3	21	1	BOH1_BOMVA	P82282 bombina var
22	20	30.3	21	1	BOH4_BOMVA	P82284 bombina var
23	20	30.3	21	1	BOH5_BOMVA	P82285 bombina var
24	20	30.3	21	1	MDH_KLEPN	P80535 klebsiella
25	20	30.3	22	1	BS23_SERPL	P83378 serratia pl
26	20	30.3	22	1	MLP_RANTE	P56924 rana tempor
27	20	30.3	24	1	PS1_PSEPD	P83188 pseudis par
28	19	28.8	10	1	TEMY_RANTE	P56923 rana tempor
29	19	28.8	14	1	MAST_VESXA	P01515 vespa xanth
30	19	28.8	19	1	UP25_UPEIN	P82031 uperoleia i
31	19	28.8	20	1	MAX8_BOMMX	P83087 bombina max
32	19	28.8	20	1	RT16_BOVIN	P82915 bos taurus
33	19	28.8	24	1	PRE4_LITIN	P82023 litoria inf
34	19	28.8	25	1	BLP4_BOMOR	P56924 bombina ori
35	19	28.8	25	1	CR23_LITCE	P56925 litoria cae
36	19	28.8	25	1	CR24_LITCE	P56926 litoria cae
37	19	28.8	25	1	SPIG_PSINU	P82457 pseudacanth
38	18	27.3	13	1	CRBL_VESAN	P17253 vespa analis
39	18	27.3	13	1	CRBL_VESXA	P17254 vespa xanth
40	18	27.3	13	1	BPA1_RANES	P56415 rana esculo
41	18	27.3	14	1	CRBL_VESVA	P17255 vespa velut
42	18	27.3	17	1	BCL4_MEGPE	P07495 megaderma
43	18	27.3	20	1	ARP_PIG	Q07107 sus scrofa
44	18	27.3	20	1	CPA7_PAPSP	P80855 papio sp. (
45	18	27.3	22	1	OBFX_BOVIN	P22459 bos taurus

ALIGNMENTS

RESULT 1
MCRX_METTM
ID MCRX_METTM STANDARD; PRT; 14 AA.
AC P58815;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methyl-coenzyme M reductase II alpha subunit (EC 1.8.-.-) (MCR II
DE alpha) (Fragment).
GN MRTA.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=91099370; PubMed=2269306;
RA Rospert S., Linder D., Ellermann J., Thauer R.K.;
RT "Two genetically distinct methyl coenzyme M reductases in
RT Methanobacterium thermoautotrophicum strain Marburg and delta H.";
RL Eur. J. Biochem. 194:871-877(1990).
CC -!- FUNCTION: Reduction of methyl coenzyme M (2-(methylthio)
CC ethanesulfonic acid) with 7-mercaptoheptanoylthreonine phosphate
CC to methane and an heterodisulfide.
CC -!- CATALYTIC ACTIVITY: CH(3)-S-CoM + H-S-HTP = CH(4) + CoM-S-S-HTP.
CC -!- COFACTOR: THE ENZYME COMPLEX BINDS TIGHTLY (NOT N [illegible] VALENTLY)
CC TO TWO MOLECULES OF COENZYME F430. EACH IS A YELLOW NICKEL
CC PORPHINOID.
CC -!- PATHWAY: Methanogenesis; last step.
CC -!- SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO GAMMA CHAINS.
CC -!- DEVELOPMENTAL STAGE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA.
CC MCR II IS EXPRESSED IN THE EARLY [illegible] WITH PHASE. LATE [illegible]
CC CONTAINS MOSTLY MCR I.
KW Methanogenesis; Oxidoreductase; Multigene family.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1718 MW; [illegible] CRC64;

Query Match 39.4%; Score 26; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 KALLKALK 13
| ||||
Db 7 KILLEALE 12

RESULT 2
MAST_VESCR
ID MAST_VESCR STANDARD; PRT; 14 AA.
AC P01516;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mastoparan C.
OS Vespa crabro (European hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

```
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Vespidae; Vespinae; Vespa.
OX   NCBI_TaxID=7445;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=84289390; PubMed=6206053;
RA   Argiolas A., Pisano J.J.;
RT   "Isolation and characterization of two new peptides, mastoparan C and
RT   crabrolin, from the venom of the European hornet, Vespa crabro.";
RL   J. Biol. Chem. 259:10106-10111(1984).
CC   -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC       that couple to phospholipase C.
DR   PIR; A01779; QMVHP2.
KW   Mast cell degranulation; Amidation.
FT   MOD_RES       14      14       AMIDATION.
SQ   SEQUENCE   14 AA;  1508 MW;  550C0ECA1D6AB1D7 CRC64;

  Query Match             37.9%;  Score 25;  DB 1;  Length 14;
  Best Local Similarity   54.5%;  Pred. No. 3.3e+02;
  Matches    6;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 LKALLKALKAL 15
              ||||   | :
Db          3 LKALLAVAKKI 13


RESULT 3
MAST_VESLE
ID   MAST_VESLE     STANDARD;      PRT;     14 AA.
AC   P01514;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Mastoparan.
OS   Vespula lewisii (Yellow jacket) (Wasp).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Vespidae; Vespinae; Vespula.
OX   NCBI_TaxID=7452;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Venom;
RX   MEDLINE=80155837; PubMed=540362;
RA   Hirai Y., Yasuhara T., Yoshida H., Nakajima T., Fujino M., Kitada C.;
RT   "A new mast cell degranulating peptide 'mastoparan' in the venom of
RT   Vespula lewisii.";
RL   Chem. Pharm. Bull. 27:1942-1944(1979).
CC   -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC       that couple to phospholipase C.
DR   PIR; A01776; QMWAVV.
DR   PDB; 1D7N; 20-JUN-01.
KW   Mast cell degranulation; Amidation; 3D-structure.
FT   MOD_RES       14      14       AMIDATION.
SQ   SEQUENCE   14 AA;  1480 MW;  CC0C0ECA1D7B00DD CRC64;

  Query Match             37.9%;  Score 25;  DB 1;  Length 14;
  Best Local Similarity   60.0%;  Pred. No. 3.3e+02;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 KALKALLKAL 12
              ||| | | | :
Db          4 KAIAAIAKKI 13


RESULT 4
MAST_VESMA
ID   MAST_VESMA     STANDARD;      PRT;     14 AA.
AC   P04205;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Mastoparan M (Mast cell-degranulating peptide).
OS   Vespa mandarinia (Hornet).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Vespidae; Vespinae; Vespa.
OX   NCBI_TaxID=7446;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RA   Hirai Y., Yasuhara T., Yoshida H., Nakajima T.;
RT   "A new mast cell degranulating peptide, mastoparan M, in the venom of
RT   the hornet Vespa mandarinia.";
RL   Biomed. Res. 2:447-449(1981).
CC   -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC       that couple to phospholipase C.
DR   PIR; A01777; QMVHMM.
KW   Mast cell degranulation; Amidation.
FT   MOD_RES       14      14       AMIDATION.
SQ   SEQUENCE   14 AA;  1480 MW;  C05A7ECA1D7B00DA CRC64;

  Query Match             37.9%;  Score 25;  DB 1;  Length 14;
  Best Local Similarity   60.0%;  Pred. No. 3.3e+02;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 KALKALLKAL 12
              ||: || | |
Db          4 KAIAALAKKL 13


RESULT 5
PCW6_PACGO
ID   PCW6_PACGO     STANDARD;      PRT;     20 AA.
AC   P82428;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ponericin W6.
OS   Pachycondyla goeldii (Ponerine ant).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicoidea;
OC   Ponerinae; Pachycondyla.
OX   NCBI_TaxID=118088;
RN   [1]
RP   SEQUENCE, FUNCTION, AND AMIDATION.
RC   TISSUE=Venom;
RX   MEDLINE=21265562; PubMed=11279030;
RA   Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA   Longeon A., Chafotte A., Dejean A., Rossier J.;
RT   "Ponericins, new antibacterial and insecticidal peptides from the
RT   venom of the ant Pachycondyla goeldii.";
RL   J. Biol. Chem. 276:17823-17829(2001).
CC   -!- FUNCTION: ACTIVITY AGAINST GRAM-POSITIVE BACTERIA, HAS
CC       INSECTICIDAL AND HEMOLYTIC ACTIVITIES.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- MASS SPECTROMETRY: MW=2029.49; METHOD=MALDI.
KW   Antibiotic; Insect immunity; Hemolysis; Amidation.
FT   MOD_RES       20      20       AMIDATION.
SQ   SEQUENCE   20 AA;  2030 MW;  5241E1528A9A08EB CRC64;

  Query Match             37.9%;  Score 25;  DB 1;  Length 20;
  Best Local Similarity   41.7%;  Pred. No. 4.6e+02;
  Matches    5;  Conservative    4;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          2 AKALKALLKALK 13
              | |: |::|  |
Db          9 ASAIPAIVKLFK 20


RESULT 6
B0MN_B0MVA
ID   B0MN_B0MVA     STANDARD;      PRT;     24 AA.
AC   P01505;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
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DT   15-SEP-2004 (Rel. 42, Last annotation update)
DE   Bombinin.
OS   Bombina variegata (Yellow-bellied toad).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX   NCBI_TaxID=8348;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RA   Csordas A., Michl H.;
RT   "Isolation and structural resolution of a haemolytically active
RT   polypeptide from the immune secretion of a European toad.";
RL   Monatsh. Chem. 101:182-189(1970).
CC   -!- FUNCTION: Has antimicrobial and hemolytic activities.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
DR   PIR; A01766; BMTD.
KW   Amphibian defense peptide; Antibiotic; Hemolysis; Amidation.
FT   MOD_RES      24     24       AMIDATION.
SQ   SEQUENCE   24 AA;  2294 MW;  ACC0FCE3B7402E85 CRC64;

  Query Match             37.9%;  Score 25;  DB 1;  Length 24;
  Best Local Similarity   66.7%;  Pred. No. 5.5e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 ALKALLKAL 12
              ||| | | |
Db         10 ALKGLAKGL 18


RESULT 7
MAST_VESOR
ID   MAST_VESOR      STANDARD;      PRT;     14 AA.
AC   P17238;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Mastoparan (Histamine releasing peptide 1) (HR-I).
OS   Vespa orientalis (oriental hornet).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Vespidae; Vespinae; Vespa.
OX   NCBI_TaxID=7447;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RA   Miroshnikov A.I., Snezhkov E.V., Nazimov I.V., Reshetova O.I.,
RA   Rozynov B.V., Gushchin I.S.;
RT   "Structure and properties of histamine releasing peptides from the
RT   venom of Vespa orientalis hornet.";
RL   Bioorg. Khim. 7:1467-1477(1981).
CC   -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC       that couple to phospholipase C.
DR   PIR; JN0389; JN0389.
KW   Mast cell degranulation; Amidation.
FT   MOD_RES      14     14       AMIDATION.
SQ   SEQUENCE   14 AA;  1494 MW;  C84F9ECA026B00DD CRC64;

  Query Match             36.4%;  Score 24;  DB 1;  Length 14;
  Best Local Similarity   62.5%;  Pred. No. 4.8e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 KALKALLK 10
              ||: ||:|
Db          4 KAIAALVK 11


RESULT 8
CHEP_PARID
ID   CHEP_PARID      STANDARD;      PRT;     13 AA.
AC   P42718;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Chemotactic peptide.
OS   Parapolybia indica.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Vespidae; Polistinae; Parapolybia.
OX   NCBI_TaxID=31921;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RA   Toki T., Yasuhara T., Nakajima T.;
RT   "Isolation and sequential analysis of peptides on the venom sac of
RT   Parapolybia indica.";
RL   Eisei Dobutsu 39:105-111(1988).
KW   Chemotaxis; Amidation.
FT   MOD_RES      13     13       AMIDATION.
SQ   SEQUENCE   13 AA;  1298 MW;  5C9505E8E39D5873 CRC64;

  Query Match             34.8%;  Score 23;  DB 1;  Length 13;
  Best Local Similarity   62.5%;  Pred. No. 6.5e+02;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 LLKALKAL 15
              ||| : ||
Db          4 LLKGISAL 11


RESULT 9
VI01_VACCV
ID   VI01_VACCV      STANDARD;      PRT;     20 AA.
AC   P16714;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Protein 11 (Fragment).
GN   11L.
OS   Vaccinia virus (strain WR).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10254;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88215015; PubMed=2835495;
RA   Schmitt J.F.C., Stunnenberg H.G.;
RT   "Sequence and transcriptional analysis of the vaccinia virus HindIII
RT   I fragment.";
RL   J. Virol. 62:1889-1897(1988).
CC   -!- SIMILARITY: BELONGS TO THE POXVIRUSES 11 FAMILY.
CC   ----------- ---- ---- ---- -- ---- ---- ---- ---- ---- ---- ----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------- ---- ---- ---- -- ---- ---- ---- ---- ---- ---- ----
DR   EMBL; J03399; AAB59803.1; -.
DR   InterPro; IPR004969; Pox_11.
DR   Pfam; PF03289; Pox_11; 1.
KW   Late protein.
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2241 MW;  6E97AA78D505C481 CRC64;

  Query Match             34.8%;  Score 23;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.6e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AKALKA 7
              |:|||
Db         15 ARALKA 20
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RESULT 10
RS19_ASHYP
ID   RS19_ASHYP     STANDARD;      PRT;    13 AA.
AC   Q44562;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   30S ribosomal protein S19 (Fragment).
GN   RPSS OR RPS19.
OS   Ash yellows phytoplasma.
OC   Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC   Acholeplasmataceae; Phytoplasma.
OX   NCBI_TaxID=35780;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94350802; PubMed=8071198;
RA   Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT   "Phylogeny of mycoplasmalike organisms (phytoplasmas): a basis for
RT   their classification.";
RL   J. Bacteriol. 176:5244-5254(1994).
CC   -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC       TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L26909; AAA83936.1; -.
DR   HAMAP; MF_00531; -; 1.
DR   InterPro; IPR002222; Ribosomal_S19.
DR   PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW   Ribosomal protein; rRNA-binding.
FT   NON_TER       1       1
SQ   SEQUENCE   13 AA;  1433 MW;  CECA010B84E6405D CRC64;

  Query Match             33.3%;  Score 22;  DB 1;  Length 13;
  Best Local Similarity   66.7%;  Pred. No. 9.3e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 LLKALK 13
              |||:|
Db          3 LLKAIK 8


RESULT 11
JAP2_RANJA
ID   JAP2_RANJA     STANDARD;      PRT;    21 AA.
AC   P83306;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2004 (Rel. 42, Last annotation update)
DE   Japonicin-2.
OS   Rana japonica (Japanese reddish frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8402;
RN   [1]
RP   SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RX   MEDLINE=21826910; PubMed=11835990;
RA   Isaacson T., Soto A., Iwamuro S., Knoop F.C., Conlon J.M.;
RT   "Antimicrobial peptides with atypical structural features from the
RT   skin of the Japanese brown frog Rana japonica.";
RL   Peptides 23:419-425(2002).
CC   -!- FUNCTION: Antibacterial activity against the Gram-negative
CC       bacterium E.coli and the Gram positive bacterium S.aureus.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- MASS SPECTROMETRY: MW=2095.4; METHOD=Electrospray.
KW   Amphibian defense peptide; Antibiotic.
FT   DISULFID     14     21       BY SIMILARITY.
SQ   SEQUENCE   21 AA;  2378 MW;  A0C5BB0C7A6CB81 CRC64;

  Query Match             33.3%;  Score 22;  DB 1;  Length 21;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+03;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 KALKALK 10
              ||| |||
Db          11 KALCILK 18


RESULT 12
PCL1_PACGO
ID   PCL1_PACGO     STANDARD;      PRT;    24 AA.
AC   P82421;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ponericin L1.
OS   Pachycondyla goeldii (Ponerine ant).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae
OC   Ponerinae; Pachycondyla.
OX   NCBI_TaxID=118888;
RN   [1]
RP   SEQUENCE, FUNCTION, AND AMIDATION.
RC   TISSUE=Venom;
RX   MEDLINE=21264562; PubMed=11290565;
RA   Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA   Longeon A., Chaffotte A., Dejean A., Rossier J.;
RT   "Ponericins, new antibacterial and insecticidal peptides from the
RT   venom of the ant Pachycondyla goeldii.";
RL   J. Biol. Chem. 276:17823-17829(2001).
CC   -!- FUNCTION: BROAD SPECTRUM ANTIBIOTIC ACTIVITY AGAINST BOTH GRAM-
CC       AND GRAM-NEGATIVE BACTERIA. HAS NON HEMOLYTIC ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- MASS SPECTROMETRY: MW=2094.7; METHOD=MALDI.
KW   Antibiotic; Insect immunity; Amidation.
FT   MOD_RES      24      24       AMIDATION.
SQ   SEQUENCE   24 AA;  2599 MW;  2A4A6B72657EB5A CRC64;

  Query Match             33.3%;  Score 22;  DB 1;  Length 24;
  Best Local Similarity   50.0%;  Pred. No. 1.6e+03;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 KALKALKAL 15
              |||:  :|:|
Db          14 KAVLGKIKGL 23


RESULT 13
PCL2_PACGO
ID   PCL2_PACGO     STANDARD;      PRT;    24 AA.
AC   P82422;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ponericin L2.
OS   Pachycondyla goeldii (Ponerine ant).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae
OC   Ponerinae; Pachycondyla.
OX   NCBI_TaxID=118888;
RN   [1]
RP   SEQUENCE, FUNCTION, AND AMIDATION.
RC   TISSUE=Venom;
RX   MEDLINE=21264562; PubMed=11290565;
RA   Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA   Longeon A., Chaffotte A., Dejean A., Rossier J.;
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RT   "Ponericins, new antibacterial and insecticidal peptides from the
RT   venom of the ant Pachycondyla goeldii.";
RL   J. Biol. Chem. 276:17822-17829(2001).
CC   -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
CC       AND GRAM-NEGATIVE BACTERIA. HAS NON-HEMOLYTIC ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- MASS SPECTROMETRY: MW=2576.67; METHOD=MALDI.
KW   Antibiotic; Insect immunity; Amidation.
FT   MOD_RES      24      24       AMIDATION.
SQ   SEQUENCE   24 AA;  2578 MW;  37830D57B1515E8F CRC64;

  Query Match             33.3%;  Score 22;  DB 1;  Length 24;
  Best Local Similarity   50.0%;  Pred. No. 1.6e+03;
  Matches    5;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          6 KALLKALKAL 15
              ||:|  :| |
Db         14 KAVLGKIKGL 23


RESULT 14
PGQ_XENLA
ID   PGQ_XENLA      STANDARD;      PRT;    24 AA.
AC   P39080;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Antimicrobial peptide PGQ.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Stomach;
RX   MEDLINE=92011794; PubMed=1717472;
RA   Moore K.S., Bevins C.L., Brasseur M.M., Tomassini N., Turner K.,
RA   Eck H., Zasloff M.;
RT   "Antimicrobial peptides in the stomach of Xenopus laevis.";
RL   J. Biol. Chem. 266:19851-19857(1991).
CC   -!- FUNCTION: ANTIMICROBIAL PEPTIDE.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: IS SYNTHESIZED IN THE STOMACH AND STORED
CC       IN A NOVEL GRANULAR MULTINUCLEATED CELL IN THE GASTRIC MUCOSA.
CC       IT IS STORED AS ACTIVE, PROCESSED PEPTIDES IN LARGE GRANULES
CC       WITHIN THE GRANULAR GLAND SECRETIONS OF THE SKIN.
CC   -!- SIMILARITY: BELONGS TO THE MAGAININ FAMILY OF ANTIMICROBIAL
CC       PEPTIDES.
DR   PIR; A41037; A41037.
KW   Amphibian defense peptide; Antibiotic.
SQ   SEQUENCE   24 AA;  2457 MW;  7E6A87CB7CF22B9C CRC64;

  Query Match             33.3%;  Score 22;  DB 1;  Length 24;
  Best Local Similarity   71.4%;  Pred. No. 1.6e+03;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ALKALLK 10
              || |:||
Db         17 ALNAVLK 23


RESULT 15
ALRX_PSEPU
ID   ALRX_PSEPU     STANDARD;      PRT;    16 AA.
AC   P17916;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Broad-specificity amino acid racemase (EC 5.1.1.-) (Fragment).
OS   Pseudomonas putida.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=303;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=AKU 0813;
RX   MEDLINE=85072910; PubMed=6439237;
RA   Roise D., Soda K., Yagi T., Walsh C.T.;
RT   "Inactivation of the Pseudomonas striata broad specificity amino acid
RT   racemase by D and L isomers of beta substituted alanines: kinetics,
RT   stoichiometry, active site peptide, and mechanistic studies.";
RL   Biochemistry 23:5195-5201(1984).
CC   -!- COFACTOR: Pyridoxal phosphate.
CC   -!- SIMILARITY: Belongs to the alanine racemase family.
DR   PIR; A29523; A29520.
DR   HAMAP; MF_01201; atypical; 1.
DR   InterPro; IPR000821; Ala_racemase.
DR   PROSITE; PS00395; ALANINE_RACEMASE; 1.
KW   Isomerase; Pyridoxal phosphate.
FT   NON_TER       1       1
FT   ACT_SITE      6       6       CATALYTIC BASE SPECIFIC FOR L-ALANINE (BY
FT                                 SIMILARITY).
FT   BINDING       6       6       PYRIDOXAL PHOSPHATE.
FT   NON_TER      16      16
SQ   SEQUENCE   16 AA;  1572 MW;  BC6C27DA1042B2B7 CRC64;

  Query Match             31.8%;  Score 21;  DB 1;  Length 16;
  Best Local Similarity   71.4%;  Pred. No. 1.6e+04;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 LKALLKA 11
              | |:|||
Db          1 LTAVLKA 7


RESULT 16
Y194_ARCFU
ID   Y194_ARCFU     STANDARD;      PRT;    25 AA.
AC   O30045;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein AF0194.
GN   AF0194.
OS   Archaeoglobus fulgidus.
OC   Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC   Archaeoglobaceae; Archaeoglobus.
OX   NCBI_TaxID=2234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX   MEDLINE=98389475; PubMed=9689475;
RA   Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA   Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA   Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA   Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA   Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA   Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA   Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA   Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA   Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA   Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA   Venter J.C.;
RT   "The complete genome sequence of the hyperthermophilic, sulphate
RT   reducing archaeon Archaeoglobus fulgidus.";
RL   Nature 390:364-370(1997).
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
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DR   EMBL; AF001093; AAB91054.1; -.
DR   PIR; B69274; B69274.
DR   TIGR; AF0194; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   25 AA;  2828 MW;  9F480F03C367419F CRC64;

  Query Match             31.8%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   57.1%;  Pred. No. 2.4e+03;
  Matches    4;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 KALLKAL 12
              |:||:|
Db          4 KAVLKGM 10


RESULT 17
UP36_UPEMJ
ID   UP36_UPEMJ      STANDARD;      PRT;    17 AA.
AC   P82044;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-SEP-2004 (Rel. 42, Last annotation update)
DE   Uperin 3.6.
OS   Uperoleia mjobergii (Australian toadlet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Myobatrachinae; Uperoleia.
OX   NCBI_TaxID=104954;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RA   Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "New antibiotic uperin peptides from the dorsal glands of the
RT   australian toadlet Uperoleia mjobergii.";
RL   Aust. J. Chem. 49:1325-1331(1996).
CC   -!- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
CC       L.INNOCUA, M.LUTEUS, S.AUREUS, S.EPIDERMIS AND S.ORERIS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC   -!- MASS SPECTROMETRY: MW=1826; METHOD=FAB.
KW   Amphibian defense peptide; Antibiotic; Amidation.
FT   MOD_RES      17     17       AMIDATION.
SQ   SEQUENCE   17 AA;  1778 MW;  784D8BB46263CA3D CRC64;

  Query Match             30.4%;  Score 20;  DB 1;  Length 17;
  Best Local Similarity   41.7%;  Pred. No. 2.5e+03;
  Matches    5;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 ALKALLKALKAL 15
              | |  :  | | |
Db          5 AAKKVVNVLKNL 16


RESULT 18
OBP_LYMDI
ID   OBP_LYMDI       STANDARD;      PRT;    18 AA.
AC   P34174;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   General odorant-binding protein (GOBP) (Fragment).
OS   Lymantria dispar (Gypsy moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC   Lymantriidae; Lymantria.
OX   NCBI_TaxID=13124;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=91186129; PubMed=2010751;
RA   Vogt R.G., Prestwich G.D., Lerner M.R.;
RT   "Odorant-binding-protein subfamilies associate with distinct classes
RT   of olfactory receptor neurons in insects.";
RL   J. Neurobiol. 22:74-84(1991).
CC   -!- FUNCTION: PRESENT IN THE AQUEOUS PHASE SURROUNDING THE
CC       SENSORY DENDRITES AND ARE THOUGHT TO BE INVOLVED IN
CC       TRANSPORT OF HYDROPHOBIC ODORANTS INTO AND THROUGH THE LYMPH.
CC   -!- SUBUNIT: Homodimer (Probable).
CC   -!- TISSUE SPECIFICITY: ANTENNA.
CC   -!- SIMILARITY: BELONGS TO THE PBP/GOBP FAMILY.
KW   Olfaction; Transport.
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  1964 MW;  BEBA1B08FD0ec2A CRC64;

  Query Match             30.4%;  Score 20;  DB 1;  Length 18;
  Best Local Similarity   66.7%;  Pred. No. 2.6e+03;
  Matches    4;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FAKALK 6
              | |:|:
Db         12 FGKALE 17


RESULT 19
JHBP_BOMMO
ID   JHBP_BOMMO      STANDARD;      PRT;    20 AA.
AC   P81627;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Juvenile hormone binding protein (Fragment).
GN   JHBP.
OS   Bombyx mori (Silk moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC   Bombycidae; Bombyx.
OX   NCBI_TaxID=7091;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=Backokjam; TISSUE=Hemolymph;
RA   Park C., Kim H.R.;
RT   "Characterization of high affinity juvenile hormone binding protein
RT   the hemolymph of Bombyx mori L.";
RL   Taehan Nanghae Chi 37:495-503(1994).
RN   [2]
RP   IDENTIFICATION OF CYS 9.
RA   Park C. H.;
RL   Submitted (DEC-1998) to the SWISS-PROT data bank.
CC   -!- FUNCTION: PREVENTS JUVENILE HORMONE FROM BEING BYED (LYSED) BY
CC       GENERAL ESTERASES BY COMBINING WITH IT STOICHIOMETRICALLY.
CC   -!- SUBCELLULAR LOCATION: Secreted.
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2060 MW;  B43633ZF6AE2FB4 CRC64;

  Query Match             30.4%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 2.8e+03;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 ALLKALK 13
              |||: |
Db          4 ALLKPLK 10


RESULT 20
SYR_RAT
ID   SYR_RAT         STANDARD;      PRT;    20 AA.
AC   P48429;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS)
DE   (Fragment).
GN   RARS.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
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EN   1.
SE   SEQUENCE.
RX   MEDLINE=90258627; PubMed=2187187;
RA   Shiram P., Doutsches M.P.;
RT   "Existence of two forms of rat liver arginyl-tRNA synthetase suggests
RT   channeling of aminoacyl-tRNA for protein synthesis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:3665-3669(1990).
CC   -!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
CC       diphosphate + L-arginyl-tRNA(Arg).
CC   -!- SUBUNIT: MONOMER; ALSO PART OF A MULTISUBUNIT COMPLEX THAT GROUPS
CC       TRNA LIGASES (LYS, ARG, ASP, GLY, GLN, ILE, LEU, VAL, MET AND PRO).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to class I aminoacyl-tRNA synthetase family.
DR   PIR; A35897; A35897.
DR   InterPro; IPR001412; tRNA synt_1.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_1; PARTIAL.
KW   Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT   NON_TER       2      2
SQ   SEQUENCE   2 AA;  227 MW;  1C6EA1947A7EB463 CRC64;

  Query Match             30.4%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   57.1%;  Prod. No. 2.8e-03;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FAFALRA 7
              | ||:|:
Db         12 FGKAIRA 18


RESULT 21
BOH1_BOMVA
ID   BOH1_BOMVA      STANDARD;      PRT:    21 AA.
AC   P82282; P82283;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Bombinin H1/H3.
OS   Bombina variegata (Yellow-bellied toad).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX   NCBI_TaxID=8348;
RN   [1]
RP   SEQUENCE, AND POST-TRANSLATIONAL MODIFICATIONS.
RC   TISSUE=Skin secretion;
RX   MEDLINE=94038967; PubMed=8223491;
RA   Mignogna G., Simmaco M., Kreil G., Barra D.;
RT   "Antibacterial and haemolytic peptides containing D-alloisoleucine
RT   from the skin of Bombina variegata.";
RL   EMBO J. 12:4829-4832(1993).
CC   -!- FUNCTION: Has antimicrobial and hemolytic activities.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
DR   PIR; B44581; B44581.
KW   Amphibian defense peptide; Antibiotic; Hemolysis; Amidation;
KW   D-amino acid.
FT   PEPTIDE       1      20       BOMBININ H1/H3.
FT   MOD_RES       2       2       D-ALLO-ISOLEUCINE (IN BOMBININ H3).
FT   MOD_RES      20      20       AMIDATION (G-21 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   21 AA;  1994 MW;  08C728IE1BDAB6BD CRC64;

  Query Match             30.4%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   55.6%;  Prod. No. 4e-03;
  Matches    5;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 AFKALLKAL 12
              |:|:|:|:|
Db         12 AIGDLLKKI 20


RESULT 22
BOH4_BOMVA
ID   BOH4_BOMVA      STANDARD;      PRT:    21 AA.
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AC   P82284;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Bombinin H4.
OS   Bombina variegata (Yellow-bellied toad).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX   NCBI_TaxID=8348;
RN   [1]
RP   SEQUENCE, AND POST-TRANSLATIONAL MODIFICATIONS.
RC   TISSUE=Skin secretion;
RX   MEDLINE=94038967; PubMed=8223491;
RA   Mignogna G., Simmaco M., Kreil G., Barra D.;
RT   "Antibacterial and haemolytic peptides containing D-alloisoleucine
RT   from the skin of Bombina variegata.";
RL   EMBO J. 12:4829-4832(1993).
CC   -!- FUNCTION: HAS ANTIMICROBIAL AND HEMOLYTIC ACTIVITIES.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
KW   Amphibian defense peptide; Antibiotic; Hemolysis; Amidation;
KW   D-amino acid.
FT   PEPTIDE       1      20       BOMBININ H4.
FT   MOD_RES       2       2       D-ALLO-ISOLEUCINE.
FT   MOD_RES      20      20       AMIDATION (G-21 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   21 AA;  1975 MW;  08C728IE1B0BF9BE CRC64;

  Query Match             30.4%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   55.6%;  Prod. No. 4e-03;
  Matches    5;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 AFKALLKAL 12
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Db          1 ALEKKLKYL 9


RESULT 26
MLP_RANTE
ID   MLP_RANTE       STANDARD;       PRT;    22 AA.
AC   P56924;
DT   30-MAY-2000 (Rel. 39, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Melittin-like peptide (MLP).
OS   Rana temporaria (European common frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8407;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=97175058; PubMed=9022710;
RA   Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA   Barra D.;
RT   "Temporins, antimicrobial peptides from the European red frog Rana
RT   temporaria.";
RL   Eur. J. Biochem. 242:788-792(1996).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: HIGH, TO A.MELLIFERA MELITTIN.
KW   Amphibian defense peptide; Amidation.
FT   MOD_RES      22     22       AMIDATION.
SQ   SEQUENCE   22 AA;  2314 MW;  09963202F9B6720C CRC64;

  Query Match             30.3%;  Score 20;  DB 1;  Length 22;
  Best Local Similarity   41.7%;  Pred. No. 3.1e+03;
  Matches    5;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

QY          4 ALKALLKALKAL 15
              |||  |   | :|
Db          5 ALKVLAGVLPSI 16


RESULT 27
PSI_PSEPD
ID   PSI_PSEPD       STANDARD;       PRT;    24 AA.
AC   P83188;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Psoudin 1.
OS   Pseudis paradoxa (Paradoxical frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Pseudidae;
OC   Pseudis.
OX   NCBI_TaxID=43558;
RN   [1]
RP   SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RX   MEDLINE=21547799; PubMed=11689069;
RA   Olson S. III, Soto A.M., Knaap P.P., Chalen J.M.;
RT   "Pseudin-2: an antimicrobial peptide with low hemolytic activity from
RT   the skin of the paradoxical frog.";
RL   Biochem. Biophys. Res. Commun. 288:1001-1005(2001).
CC   -!- FUNCTION: Possesses antifungal activity against Candida and is
CC       also active against E.coli and S.aureus.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- MASS SPECTROMETRY: MW=2715.4, METHOD=Electrospray.
DR   GO; GO:0003799; F:antifungal peptide activity; IDA.
KW   Amphibian defense peptide; Fungicide; Antibiotic.
SQ   SEQUENCE   24 AA;  2715 MW;  5B62A1AB0451EB99 CRC64;
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  Query Match             30.8%;  Score 20;  DB 1;  Length 24;
  Best Local Similarity   30.8%;  Pred. No. 3.4e+03;
  Matches    4;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 KALKALLKALKAL 15
              | : : | ||| : :
Db          7 KVFQGLIHKAIKLI 19


RESULT 29
IEMK_RANTE
ID   IEMK_RANTE     STANDARD;      PRT;    19 AA.
AC   P56923;
DT   30-MAY-2000 (Rel. 39, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Temporin K.
OS   Rana temporaria (European common frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8407;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=97175050; PubMed=9022710;
RA   Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA   Barra D.;
RT   "Temporins, antimicrobial peptides from the European red frog Rana
RT   temporaria.";
RL   Eur. J. Biochem. 242:788-792(1996).
CC   -!- FUNCTION: Has antibacterial activity against Gram-positive
CC       bacteria.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: Belongs to the brevinin family.
KW   Amphibian defense peptide; Antibiotic; Amidation.
FT   MOD_RES       10      10       AMIDATION.
SQ   SEQUENCE   10 AA;  1122 MW;  3605A9B237272457 CRC64;

  Query Match             28.8%;  Score 19;  DB 1;  Length 10;
  Best Local Similarity   62.5%;  Pred. No. 2.2e+03;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 LKALLKAL 12
              | :|:|:|
Db          2 IPNLLKSL 9


RESULT 30
MAST_VESXA
ID   MAST_VESXA     STANDARD;      PRT;    14 AA.
AC   P01515;
DT   01-JUL-1986 (Rel. 01, Created)
DT   01-JUL-1986 (Rel. 01, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Mastoparan X (MP-X).
OS   Vespa xanthoptera (Japanese hornet).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Vespidae; Vespinae; Vespa.
OX   NCBI_TaxID=7448;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=81155378; PubMed=6403863;
RA   Hirai Y., Kiwada H., Yasuhara T., Yoshida H., Nakajima T.;
RT   "A new mast cell degranulating peptide homologous to mastoparan in
RT   the venom of Japanese hornet (Vespa xanthoptera).";
RL   Chem. Pharm. Bull. 27:1945-1946(1979).
RN   [2]
RP   STRUCTURE BY NMR.
RX   MEDLINE=92304942; PubMed=1610814;
RA   Wakamatsu K., Okada A., Miyazawa T., Ohya M., Higashijima T.;
RT   "Membrane-bound conformation of mastoparan X, a G-protein activating
RT   peptide.";
RL   Biochemistry 31:5654-5660(1992).
RN   [3]
RP   STRUCTURE BY NMR.
RX   MEDLINE=98206894; PubMed=9537994;
RA   Fujimoto H., Wakamatsu K., Sato K., Miyazawa T., Kohno T.;
RT   "G protein-bound conformation of mastoparan X: heteronuclear
RT   multidimensional transferred nuclear overhauser effect analysis of
RT   peptide uniformly enriched with 13C and 15N.";
RL   Biochemistry 37:4782-4790(1998).
CC   -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC       that couple to phospholipase C.
DR   PIR; A01778; QMVHXX.
DR   PDB; 1A13; 16-FEB-99.
KW   Mast cell degranulation; Amidation; 3D structure.
FT   MOD_RES       14      14       AMIDATION.
SQ   SEQUENCE   14 AA;  1557 MW;  C85DE0D7AA7AB0DD CRC64;

  Query Match             28.8%;  Score 19;  DB 1;  Length 14;
  Best Local Similarity   40.0%;  Pred. No. 4e+03;
  Matches    4;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 KALKALLKAL 12
              | : |: | |
Db          4 KGIAAMAKKL 13


RESULT 30
UP25_UPEIN
ID   UP25_UPEIN     STANDARD;      PRT;    19 AA.
AC   P82031;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Uperin 2.5.
OS   Uperoleia inundata (Floodplain toadlet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Myobatrachinae; Uperoleia.
OX   NCBI_TaxID=104953;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RA   Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
RA   Adams G.W., Severini C.;
RT   "Novel uperin peptides from the dorsal glands of the australian
RT   floodplain toadlet Uperoleia inundata.";
RL   Aust. J. Chem. 49:475-484(1996).
CC   -!- FUNCTION: SHOWS A MEDIUM ANTIBACTERIAL ACTIVITY AGAINST M.LUTEUS,
CC       L.MESENTEROIDES AND S.UBERIS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC    !  TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC   -!- MASS SPECTROMETRY: MW=1940; METHOD=FAB.
KW   Amphibian defense peptide; Antibiotic.
SQ   SEQUENCE   19 AA;  1941 MW;  5E94C6C75784643D9 CRC64;

  Query Match             28.8%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   40.0%;  Pred. No. 5.9e+03;
  Matches    4;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLK 10
              |:| :  : |
Db          5 FAKGVLGKIK 14


RESULT 31
MAX8_BOMMX
ID   MAX8_BOMMX     STANDARD;      PRT;    20 AA.
AC   P83087;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
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                                    (Rel. 41, Last annotation update)
ID   MAK16_XENLA             STANDARD;      PRT;     ... AA.
AC   ...;
DT   ... (Rel. 39, Created)
DT   ... (Rel. 39, Last sequence update)
DT   ... (Rel. 41, Last annotation update)
DE   ... ribosomal protein S16 (MRP-S16) (Fragments).
GN   ...
OS   ... (African clawed frog).
OC   ... Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   ... Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopus.
OX   ...
RN   [1]
RP   ...
RX   ...
RA   ...
RT   ...
RL   ...
CC   -!- FUNCTION: ...
CC   -!- SUBCELLULAR LOCATION: ...
CC   -!- SIMILARITY: ...
DR   ...
KW   ...
SQ   SEQUENCE   ... AA;  ... MW;  ... CRC64;

  Query Match          ...%;  Score ...;  DB ...;  Length ...;
  Best Local Similarity   ...%;  Pred. No. ...;
  Matches   ...;  Conservative   ...;  Mismatches   ...;  Indels   ...;  Gaps   ...;

Qy          ... FAKALKALLK ...
                    ...
Db          ... ALRRLK ...


RESULT ...
...
ID   ... STANDARD;      PRT;     ... AA.
AC   ...;
DT   ... (Rel. 40, Created)
DT   ... (Rel. 40, Last sequence update)
DT   ... (Rel. 41, Last annotation update)
DE   ... ribosomal protein S16 (MRP-S16) (Fragments).
GN   ...
OS   ... (African clawed frog).
OC   ... Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   ... Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopus.
OX   ...
RN   [1]
RP   ...
RX   ...
RA   ...
RT   ...
RL   ...
CC   -!- FUNCTION: ...
CC   -!- SUBCELLULAR LOCATION: ...
CC   -!- SIMILARITY: ...
DR   ...
KW   ...
SQ   SEQUENCE   ... AA;  ... MW;  ... CRC64;

  Query Match          ...%;  Score ...;  DB ...;  Length ...;
  Best Local Similarity   ...%;  Pred. No. ...;
  Matches   ...;  Conservative   ...;  Mismatches   ...;  Indels   ...;  Gaps   ...;

Qy          ... FAKALKALLK ...
                    ...
Db          ... ALRRLK ...


RESULT ...
...
ID   ... STANDARD;      PRT;     ... AA.
AC   ...;
DT   ... (Rel. 40, Created)
DT   ... (Rel. 40, Last sequence update)
DT   ... (Rel. 41, Last annotation update)
DE   ... ribosomal protein S16 (MRP-S16) (Fragments).
GN   ...
OS   ... (African clawed frog).
OC   ... Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   ... Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopus.
OX   ...
RN   [1]
RP   ...
RX   ...
RA   ...
RT   ...
RL   ...
CC   -!- FUNCTION: ...
CC   -!- SUBCELLULAR LOCATION: ...
CC   -!- SIMILARITY: ...
DR   ...
KW   ...
SQ   SEQUENCE   ... AA;  ... MW;  ... CRC64;

  Query Match          ...%;  Score ...;  DB ...;  Length ...;
  Best Local Similarity   ...%;  Pred. No. ...;
  Matches   ...;  Conservative   ...;  Mismatches   ...;  Indels   ...;  Gaps   ...;

Qy          ... FAKALKALLK ...
                    ...
Db          ... ALRRLK ...


RESULT ...
...
ID   ... STANDARD;      PRT;     ... AA.
AC   ...;
DT   ... (Rel. 39, Created)
DT   ... (Rel. 39, Last sequence update)
DT   ... (Rel. 41, Last annotation update)
DE   ... ribosomal protein S16 (MRP-S16) (Fragments).
GN   ...
OS   ... (African clawed frog).
OC   ... Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   ... Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopus.
OX   ...
RN   [1]
RP   ...
RX   ...
RA   ...
RT   ...
RL   ...
CC   -!- FUNCTION: ...
CC   -!- SUBCELLULAR LOCATION: ...
CC   -!- SIMILARITY: ...
DR   ...
KW   ...
SQ   SEQUENCE   ... AA;  ... MW;  ... CRC64;

  Query Match          ...%;  Score ...;  DB ...;  Length ...;
  Best Local Similarity   ...%;  Pred. No. ...;
  Matches   ...;  Conservative   ...;  Mismatches   ...;  Indels   ...;  Gaps   ...;

Qy          ... FAKALKALLK ...
                    ...
Db          ... ALRRLK ...


RESULT 33
PRF4_LITIN
ID   PRF4_LITIN      STANDARD;      PRT;     24 AA.
AC   PR2023;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Frenatin 4.
OS   Litoria infrafrenata (Giant tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Pelodryadinae; Litoria.
OX   NCBI_TaxID=61195;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RX   MEDLINE=97368637; PubMed=9225251;
RA   Rozek T., Wallace J.C., Bowie J.H., Tyler M.J.;
RT   "The structures of the frenatin peptides from the skin secretion of
RT   the giant tree frog Litoria infrafrenata.";
RL   J. Pept. Sci. 2:117-124(1996).
CC   -!- FUNCTION: Wide spectrum antimicrobial peptide.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral
CC       glands.
CC   -!- MASS SPECTROMETRY: MW=2165; METHOD=FAB.
KW   Amphibian defense peptide; Antibiotic.
SQ   SEQUENCE   24 AA;  2495 MW;  6986D06394780BA1 CRC64;

  Query Match          28.8%;  Score 15;  DB 1;  Length 24;
  Best Local Similarity   50.0%;  Pred. No. 4.8e+03;
  Matches    5;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLK 10
                |||.|||   :|
Db         13 FANALVNSIK 22


RESULT 34
BLP4_BOMOR
ID   BLP4_BOMOR      STANDARD;      PRT;     25 AA.
AC   P29005;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Bombinin-like peptide 4 (BLP-4).
OS   Bombina orientalis (oriental fire-bellied toad).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX   NCBI_TaxID=8346;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=92029177; PubMed=1744108;
RA   Gibson B.W., Tang D., Mandrell R., Kelly M., Spindel E.R.;
RT   "Bombinin-like peptides with antimicrobial activity from skin
RT   secretions of the Asian toad, Bombina orientalis.";
RL   J. Biol. Chem. 266:23103-23111(1991).
CC   -!- FUNCTION: HAS ANTIMICROBIAL ACTIVITY, BUT NO HEMOLYTIC ACTIVITY.
CC       PREFERENCE ON KILLING GRAM NEGATIVE NON ENTERIC BACTERIA.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
DR   PIR; D41575; D41575.
KW   Amphibian defense peptide; Antibiotic; Amidation.
FT   MOD_RES      25      25       AMIDATION.
SQ   SEQUENCE   25 AA;  2409 MW;  E97916654BE3E2C8 CRC64;

  Query Match          28.8%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   42.9%;  Pred. No. 5e+03;
  Matches    3;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy           6 KALKALL 12
                 |:|:| |
Db          11 KSIIKGL 17


RESULT 35
CR23_LITCE
ID   CR23_LITCE     STANDARD;      PRT:    25 AA.
AC   P56235; P82117;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   splendipherin (Caerin 2.3).
OS   Litoria caerulea (Green tree frog), and
OS   Litoria splendida (Magnificent tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=30344; 30345;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   SPECIES=L.caerulea; TISSUE=Parotoid gland;
RA   Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT   "Peptides from Australian frogs. The structures of the caerins from
RT   Litoria caerula.";
RL   J. Chem. Res. 138:910-936(1993).
RN   [2]
RP   SEQUENCE.
RC   SPECIES L.splendida; TISSUE=Parotoid gland, and Rostral gland;
RX   MEDLINE=99447045; PubMed=10519546;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Smith B.P.;
RT   "Aquatic sex pheromone from a male tree frog.";
RL   Nature 401:444-445(1999).
RN   [3]
RP   SEQUENCE.
RC   SPECIES L.splendida; TISSUE=Skin secretion;
RX   MEDLINE=20069871; PubMed=10601876;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Smith B.P.;
RT   "Differences in the skin peptides of the male and female Australian
RT   tree frog Litoria splendida. The discovery of the aquatic male sex
RT   pheromone splendipherin, together with Phe8 caerulein and the
RT   antibiotic peptide caerin 1.10.";
RL   Eur. J. Biochem. 267:269-275(2000).
CC   -!- FUNCTION: Acts as a male sex pheromone that attracts females in
CC       L.splendida. Has no antimicrobial activity.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC       GLANDS.
CC   -!- MASS SPECTROMETRY: MW=2364; METHOD=FAB.
KW   Amphibian defense peptide; Pheromone.
SQ   SEQUENCE   25 AA;  2366 MW;  DDDB2C36B49186B8 CRC64;

  Query Match             28.8%;  Score 19;  DB 1;  Length 25;
  Best Local Similarity   71.4%;  Pred. No. 5e-03;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           3 KALKALL 9
                 |:|  |:|
Db           8 KALGGLL 14


RESULT 36
CR24_LITCE
ID   CR24_LITCE     STANDARD;      PRT:    25 AA.
AC   P56236;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Caerin 2.4.
OS   Litoria caerulea (Green tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=30344;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Parotoid gland;
RA   Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT   "Peptides from Australian frogs. The structures of the caerins from
RT   Litoria caerula.";
RL   J. Chem. Res. 138:910-936(1993).
CC   -!- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
CC       CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
CC       DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC       GLANDS.
CC   -!- MASS SPECTROMETRY: MW=2450; METHOD=FAB.
KW   Amphibian defense peptide; Antibiotic.
SQ   SEQUENCE   25 AA;  2452 MW;  E3DB2C3504F57638 CRC64;

  Query Match             28.8%;  Score 19;  DB 1;  Length 25;
  Best Local Similarity   71.4%;  Pred. No. 5e-03;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           3 KALKALL 9
                 |:|  |:|
Db           8 KALGGLL 14


RESULT 37
SPIG_PSEUS
ID   SPIG_PSEUS     STANDARD;      PRT:    25 AA.
AC   P82357;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Spingerin.
OS   Pseudacanthotermes spiniger.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Dictyoptera; Isoptera; Termitidae;
OC   Macrotermitinae; Pseudacanthotermes.
OX   NCBI_TaxID=115113;
RN   [1]
RP   SEQUENCE, MASS SPECTROMETRY, AND FUNCTION.
RC   TISSUE=Blood, and Salivary gland;
RX   PubMed=11053427;
RA   Lamberty M., Zachary D., Lanot R., Bordereau C., Robert A.,
RA   Hoffmann J.A., Bulet P.;
RT   "Insect immunity. Constitutive expression of a cysteine-rich
RT   antifungal and a linear antibacterial peptide in a termite insect.";
RL   J. Biol. Chem. 276:4085-4092(2001).
CC   -!- FUNCTION: ACTIVE AGAINST GRAM-POSITIVE BACTERIA B.MEGATERIUM AND
CC       M.LUTEUS, GRAM-NEGATIVE BACTERIA E.COLI SBS363 AND D22,
CC       K.PNEUMONIAE, S.TYPHIMURIUM AND P.AERUGINOSA, YEAST C.ALBICANS
CC       AND FILAMENTOUS FUNGI F.CULMORUM, N.CRASSA, N.HAEMATOCOCCA AND
CC       T.VIRIDAE. INACTIVE AGAINST GRAM-POSITIVE BACTERIA B.SUBTILIS,
CC       S.PYOGENES, B.THURINGIENSIS AND S.AUREUS, GRAM-NEGATIVE BACTERIA
CC       E.CLOACAE AND E.CAROTOVORA AND FILAMENTOUS FUNGUS B.BASSIANA.
CC   -!- INDUCTION: By bacterial infection.
CC   -!- MASS SPECTROMETRY: MW=3001.8; METHOD=MALDI.
CC   -!- MISCELLANEOUS: THERE ARE THREE ISOFORMS OF SPINGERIN.
KW   Antibiotic; Fungicide.
FT   VARIANT       1      2       MISSING (IN N-3 ISOFORM).
FT   VARIANT      22     25       MISSING (IN C-4 ISOFORM).
SQ   SEQUENCE   25 AA;  3001 MW;  AA7947026426ZF60 CRC64;

  Query Match             28.8%;  Score 19;  DB 1;  Length 25;
  Best Local Similarity   50.0%;  Pred. No. 5e-03;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           8 LLKALKALL 15
                 |||  |: :
Db          12 LLKQLRIM 19
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RESULT 39
CRBL_VESAN
ID   CRBL_VESAN     STANDARD;      PRT;    14 AA.
AC   P17235;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Vespid chemotactic peptide A (VESCP A).
OS   Vespa analis (Hornet).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryqota;
OC   Neoptera; Endopteryqota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Vespidae; Vespinae; Vespa.
OX   NCBI_TaxID=7449;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RA   Yasuhara T., Nakajima T., Fukuda F., Fukase K., Morii M., Eltadi C.,
RA   Piyo K.;
RL   (In) Munekata E. (eds.);
RL   Peptide chemistry 1983, pp.185-190, Protein Research Foundation,
RL   Osaka (1984).
CC   -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC       of neutrophils.
KW   Mast cell degranulation; Chemotaxis; Amidation.
FT   MOD_RES      13     13       AMIDATION.
SQ   SEQUENCE   13 AA;  1466 MW;  C8D554365DF9238D CRC64;

  Query Match             27.3%;  Score 18;  DB 1;  Length 13;
  Best Local Similarity   62.5%;  Pred. No. 4e-03;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AKALKALL 9
              | :  |:|
Db          5 AKIIGGLL 13


RESULT 40
CRBL_VESXA
ID   CRBL_VESXA     STANDARD;      PRT;    14 AA.
AC   P17234;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Vespid chemotactic peptide X (VESCP X).
OS   Vespa xanthoptera (Japanese hornet).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryqota;
OC   Neoptera; Endopteryqota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Vespidae; Vespinae; Vespa.
OX   NCBI_TaxID=7448;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RA   Yasuhara T., Morokawa H., Suzuki N., Nakamura H., Nakajima T.;
RL   (In) Izumiya N. (eds.);
RL   Peptide chemistry 1984, pp.177-182, Protein Research Foundation,
RL   Osaka (1985).
CC   -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC       of neutrophils.
KW   Mast cell degranulation; Chemotaxis; Amidation.
FT   MOD_RES      13     13       AMIDATION.
SQ   SEQUENCE   13 AA;  1468 MW;  C8504D365DF9238D CRC64;

  Query Match             27.3%;  Score 18;  DB 1;  Length 13;
  Best Local Similarity   62.5%;  Pred. No. 4e-03;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AKALKALL 9
              | :  |:|
Db          5 AKIIGGLL 13


RESULT 41
HPA1_RANES
ID   HPA1_RANES     STANDARD;      PRT;    13 AA.
AC   P32415;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Hemolytic protein A1 (Fragment).
OS   Rana esculenta (Edible frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8401;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=90198965; PubMed=2317508;
RA   Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
RA   Barra D., Bossa F.;
RT   "Purification and characterization of bioactive peptides from skin
RT   extracts of Rana esculenta.";
RL   Biochim. Biophys. Acta 1033:318-323(1990).
CC   -!- FUNCTION: Shows hemolytic activity.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
DR   PIR; S09018; S09018.
KW   Amphibian defense peptide; Amidation; Hemolysis.
FT   MOD_RES      13     13       AMIDATION.
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1390 MW;  C6BA768B9DFE587D CRC64;

  Query Match             27.3%;  Score 18;  DB 1;  Length 13;
  Best Local Similarity   33.3%;  Pred. No. 4e-03;
  Matches    4;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKAL 12
              |  |:  :|  |
Db          1 FLPAIAGILSQL 12


RESULT 41
CRBL_VESOR
ID   CRBL_VESOR     STANDARD;      PRT;    14 AA.
AC   P17236;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Histamine releasing peptide II (HR-II).
OS   Vespa orientalis (Oriental hornet).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryqota;
OC   Neoptera; Endopteryqota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Vespidae; Vespinae; Vespa.
OX   NCBI_TaxID=7447;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RA   Miroshnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
RA   Rozynov B.V., Gushchin I.S.;
RT   "Structure and properties of histamine releasing peptides from the
RT   venom of Vespa orientalis hornet.";
RL   Bioorg. Khim. 7:1467-1477(1981).
CC   -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC       of neutrophils.
DR   PIR; JN0390; JN0390.
KW   Mast cell degranulation; Chemotaxis; Amidation.
FT   MOD_RES      14     14       AMIDATION.
SQ   SEQUENCE   14 AA;  1524 MW;  22015B4A6CEDED38 CRC64;

  Query Match             27.3%;  Score 18;  DB 1;  Length 14;
  Best Local Similarity   57.1%;  Pred. No. 4.2e-03;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 KALKALL 9
              | :| ||
Db          8 KLVKGLL 14
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RESULT 12
BOLA_MESPE
ID   BOLA_MESPE     STANDARD;      PRT:    17 AA.
AC   P17495;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   15-FEB-2003 (Rel. 41, Last annotation update)
DE   Bombolitin IV.
OS   Megabombus pennsylvanicus (American common bumblebee).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC   Apidae; Bombus.
OX   NCBI_TaxID=28043;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=85105023; PubMed=2578459;
RA   Argiolas A., Pisano J.J.;
RT   "Bombolitins, a new class of mast cell degranulating peptides from
RT   the venom of the bumblebee Megabombus pennsylvanicus.";
RL   J. Biol. Chem. 260:1437-1444(1985).
CC   -!- FUNCTION: Mast cell degranulating peptide.
DR   PIR; D22595; D22595.
KW   Mast cell degranulation.
SQ   SEQUENCE   17 AA;  1873 MW;  A64A4145148CFDFB6 CRC64;

  Query Match             27.3%;  Score 18;  DB 1;  Length 17;
  Best Local Similarity   57.1%;  Pred. No. 5e+03;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AKALKALKAL 8
              : : :
Db          8 AKLVKVLKAI 14


RESULT 13
ABP_EIAI
ID   ABP_EIAI        STANDARD;      PRT:    20 AA.
AC   Q07BC7;
DT   [-]-MAY-2007 (Rel. 50, Created)
DT   [-]-MAY-2007 (Rel. 50, Last sequence update)
DT   15-FEB-2007 (Rel. 49, Last annotation update)
DE   Amiloride-sensitive amine oxidase [copper-containing] (EC 1.4.3.6)
DE   (Diamine oxidase) (DAO) (Amiloride binding protein) (ABP)
DE   (Histaminase) (PK-DAO) (Fragment).
GN   ABP1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=91115095; PubMed=1711596;
RA   Novotny W.F., Chassande O., Baker M., Lazdunski M., Barbry P.;
RT   "Diamine oxidase is the amiloride-binding protein and is inhibited by
RT   amiloride analogs.";
RL   J. Biol. Chem. 266:23021-23026(1991).
CC   -!- FUNCTION: Catalyzes the degradation of compounds such as
CC       putrescine, histamine, spermine, and spermidine; substances
CC       involved in allergic and immune responses, cell proliferation,
CC       tissue differentiation, tumor formation, and possibly apoptosis.
CC       (By similarity).
CC   -!- CATALYTIC ACTIVITY: R'CH(2)NH(2) + H(2)O + O(2) = R'CHO + NH(3) +
CC       H(2)O(2).
CC   -!- PTM: 2 TPQ per subunit. Binds 1 copper ion and 1 topaquinone per subunit (By
CC       similarity).
CC   -!- SUBUNIT: HOMODIMER; Disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: Extracellular (By similarity).
CC   -!- PTM: 2-(2-hydroxyethyl)histidine (HEH) is generated by copper dependent
CC       autoxidation of a specific tyrosyl residue (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE COPPER/TOPAQUINONE AMINE OXIDASE FAMILY.
DR   PIR; B54410; B54410.
DR   GlycoSuiteDB; Q07BC7; -.
DR   InterPro; IPR000269; CuNH_oxidase.
DR   PROSITE; PS01164; COPPER_AMINE_OXID_1; PARTIAL.
DR   PROSITE; PS01165; COPPER_AMINE_OXID_2; PARTIAL.
KW   Oxidoreductase; Copper; Heparin-binding; TPQ.
FT   NON_TER       20      20
SQ   SEQUENCE   20 AA;  1898 MW;  4AGE313C6B2D09F CRC64;

  Query Match             27.3%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   41.7%;  Pred. No. 5.2e+03;
  Matches    5;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AAKALKALLKAL 12
              || :  :  ||:
Db          9 AAAGVAEDLKAV 20


RESULT 14
CPA7_PAPSP
ID   CPA7_PAPSP     STANDARD;      PRT:    20 AA.
AC   P80055;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Cytochrome P450 2A7 (EC 1.14.14.1) (CYPIIA7) (P450 IIA) (Coumarin 7
DE   hydroxylase) (Fragment).
GN   CYP2A7.
OS   Papio sp. (Baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Papio.
OX   NCBI_TaxID=9118;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=92174928; PubMed=1541279;
RA   Bulet-Beluche I., Boulenc X., Fabre J., Maurel P., Beaune P.;
RT   "Purification of two cytochrome P450 isozymes related to CYP2A and
RT   CYP3A gene families from monkey (baboon, Papio papio) liver
RT   microsomes. Cross reactivity with human forms.";
RL   Eur. J. Biochem. 204:641-648(1992).
CC   -!- PRODUCT: N, EXHIBITS A HIGH 7-ETHOXYCOUMARIN 7 ETHOXYLASE ACTIVITY.
CC   -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC       oxidized flavoprotein + H(2)O.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC   -!- INDUCTION: By phenobarbital.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   PROSITE; PS00086; CYPOCHROME_P450; PARTIAL.
KW   Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW   Microsome; Endoplasmic reticulum.
FT   UNSURE        14      14
FT   NON_TER       20      20
SQ   SEQUENCE   20 AA;  2005 MW;  F1E102A1B5C7C6 CRC64;

  Query Match             27.3%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   45.5%;  Pred. No. 5.2e+03;
  Matches    5;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 LKALLKALKAL 15
              : ||:  |  :
Db          8 IVALLACLIVM 18


RESULT 15
ODPX_BOVIN
ID   ODPX_BOVIN     STANDARD;      PRT:    32 AA.
AC   P22439;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-OCT-2001 (Rel. 40, Last annotation update)
DE   Pyruvate dehydrogenase protein X component (Dihydrolipoamide
```

```
 ;    Protein-binding domain of pyruvate dehydrogenase complex) (E3
 ;    binding protein) (E3BP) (protein X) (Fragment).
 N    (1X).
 ;    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 ;    Mammalia; Eutheria; Laurasiatheria; Ruminantia; Pecora; Bovidae;
 ;    Bos; Bos; Bos.
 X    NCBI_TaxID=9913;
 N    1,
 RP   (1-77).
 RX   MEDLINE=94350734; PubMed=7959136;
 RA   Neagle J., de Marcucci O., Dunbar B., Lindsay J.G.;
 RT   "Sequence of a cDNA encoding bovine pyruvate dehydrogenase complex-binding
 RT   protein: homology to the lipoate acetyltransferase (E2)
 RT   core family.";
 RL   Biochem. Biophys. Res. Commun. 204:1264-1270(1994).
 RN   [2]
 RP   SEQUENCE.
 RX   MEDLINE=95055115; PubMed=7961915;
 RA   Thekkumkara T.J., Dunbar B., Lindsay J.G.;
 RT   "Sequence of the cDNA encoding dihydrolipoamide dehydrogenase (E3) binding are
 RT   of the 2-oxo acid dehydrogenase complex and homology with the
 RT   pyruvate dehydrogenase multienzyme complex.";
 RL   FEBS Lett. 355:243-248(1994).
 CC   -!- FUNCTION: NOT REQUIRED FOR ANCHORING DIHYDROLIPOAMIDE DEHYDROGENASE
 CC       (E3) TO THE DIHYDROLIPOAMIDE TRANSACETYLASE (E2) CORE OF THE
 CC       PYRUVATE DEHYDROGENASE COMPLEXES OF EUKARYOTES, THIS SPECIFIC
 CC       BINDING IS ESSENTIAL FOR A FUNCTIONAL PDH COMPLEX.
 CC   -!- SUBUNIT: EUKARYOTIC PYRUVATE DEHYDROGENASE COMPLEXES ARE ORGANIZED
 CC       ABOUT A DODECAHEDRAL CORE OF THE OLIGOMERIC DIHYDROLIPOAMIDE ACETYL
 CC       TRANSFERASE, APOENZYMES WHICH ARE ARRANGED MULTIPLE COPIES OF PYRUVATE
 CC       DEHYDROGENASE, DIHYDROLIPOAMIDE DEHYDROGENASE AND PROTEIN X BOUND
 CC       BY NONCOVALENT BONDS.
 CC   -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC   -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
 CC   -!- SIMILARITY: Contains 1 lipoyl binding domain.
 DR   EMBL; X72841; CAA51004.
 DR   InterPro; IPR000089; Lipoyl.
 DR   PROSITE; PS50968; BIOTINYL_LIPOYL; PARTIAL.
 KW   Mitochondrion; Transit peptide.
 FT   VARIANT      10     10       P -> G.
 FT   NON_TER      77     77
 SQ   SEQUENCE   77 AA;  8764 MW;  4D0657222B27D301 CRC64;

  Query Match             27.5%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   36.4%;  Pred. No. 6.6e+03;
  Matches    4;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 AFALKALIKA 11
              |  |  |  :
Db          2 AVLLKEIMKD 12


Search completed: August 21, 2003, 08:21:15
Job time : 27 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 21, 2003, 08:14:35 ; Search time 39 Seconds
(without alignments)
36.988 Million cell updates/sec

Title: US-09-820-053A-43
Perfect score: 66
Sequence: 1 FAKALKALLKALKAL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 284578 seqs, 90168682 residues

Total number of hits satisfying chosen parameters: 4986

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	26	39.4	14	2	S13864	methyl coenzyme M
2	26	39.4	21	2	I40659	hypothetical prote
3	26	39.4	21	2	I40657	hypothetical prote
4	25	37.9	14	1	QMWAVV	mastoparan - yello
5	25	37.9	14	1	QMVHMM	mastoparan M - hor
6	25	37.9	14	1	QMVHP2	mastoparan C - Eur
7	25	37.9	21	2	B33600	glutamate-ammonia
8	25	37.9	24	1	BMID	bombinin - Bombina
9	24	36.4	14	2	JN0389	histamine-releasin
10	24	36.4	19	2	A44854	L-2,4-diaminobutyr
11	24	36.4	22	2	B35372	unidentified low M
12	23	34.8	15	2	PN0117	hemoglobin alpha c
13	23	34.8	25	2	B36944	orf3 3' of madA -
14	22	33.3	17	2	S09607	phenylalanine-tRNA
15	22	33.3	20	2	S68028	[redacted]
16	22	33.3	20	2	JP0056	ribosomal protein
17	22	33.3	21	2	S68971	hypothetical prote
18	22	33.3	22	2	B49410	t-complex polypept
19	22	33.3	24	2	B22317	threonine ammonia-
20	22	33.3	24	2	A41047	antimicrobial pept
21	22	33.3	25	2	PQ0683	photosystem I 16.1
22	21	31.8	16	2	A29520	amino-acid racemas
23	21	31.8	18	2	S21469	1H 4-oxoquinoline
24	21	31.8	18	2	S45373	translation elonga
25	21	31.8	20	2	A33160	H+-transporting tw
26	21	31.8	20	2	B33290	histone H2B - huma
27	21	31.8	20	2	A56046	urinary tract ston
28	21	31.8	22	2	A45913	plantaricin A - La
29	21	31.8	24	2	S68391	H+-transporting tw
30	21	31.8	24	2	B20554	hemocyanin subunit
31	21	31.8	25	2	PN0642	biphenyl dioxygena
32	21	31.8	25	2	B69274	hypothetical prote
33	20	30.3	14	2	S29789	hypothetical prote
34	20	30.3	15	2	PT0095	H+-transporting tw
35	20	30.3	18	2	S78767	ribosomal protein
36	20	30.3	20	2	B44581	bombinin H Met 8
37	20	30.3	20	2	A35857	arginine tRNA liga
38	20	30.3	22	2	A37335	68K surface antige
39	20	30.3	22	2	S33769	F-glycoprotein pap
40	20	30.3	23	2	A31944	cytochrome P450NMa
41	20	30.3	23	2	S34739	trans-cinnamate 4
42	20	30.3	24	2	G20554	hemocyanin subunit
43	20	30.3	25	2	B64710	hypothetical prote
44	19.5	29.5	15	2	PN0118	hemoglobin beta ch
45	19	28.8	11	2	A38841	rhodopsin homolog

ALIGNMENTS

RESULT 1
S13864
methyl coenzyme M reductase (EC 1.8. .) II alpha chain - Methanobacterium thermoauti
C;Species: Methanobacterium thermoautotrophicum
A;Variety: strain Marburg
C;Date: 19-Mar-1997 #sequence_revision 13-Sep-1998 #text_change 30-Oct-1998
C;Accession: S13864
R;Rospert, S.; Linder, D.; Ellermann, J.; Thauer, R.K.
Eur. J. Biochem. 194, 871-877, 1990
A;Title: Two genetically distinct methyl coenzyme M reductases in Methanobacterium th
A;Reference number: S13864; MUID:91099370; PMID:2269306
A;Accession: S13864
A;Molecule type: protein
A;Residues: 1-14 <ROS>
A;Experimental source: strain Marburg
C;Keywords: methanogenesis; oxidoreductase

Query Match 39.4%; Score 26; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 3.6e-02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 KALLKALK 13
| |||||
Db 5 KLPLEALK 12

RESULT 2
I40659
hypothetical protein - Clostridium cochlearium (fragment)
C;Species: Clostridium cochlearium
C;Date: 12-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 15-Oct-1999
C;Accession: I40659; S47461
R;Zelder, O.; Beatrix, B.; Leutbecher, U.; Buckel, W.
Eur. J. Biochem. 226, 577-585, 1994
A;Title: Characterization of the coenzyme-B12-dependent glutamate mutase from Clostri
A;Reference number: I40659; MUID:95094816; PMID:7880251
A;Accession: I40659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-21 <RES>
A;Cross-references: EMBL:X80997; NID:g540005; PIDN:CAA56920.1; PID:g540006

Query Match 39.4%; Score 26; DB 2; Length 21;
Best Local Similarity 53.8%; Pred. No. 5.4e-02;
Matches 7; Conservative 2; Mismatches 4; Indels 3; Gaps 0;

Qy 3 KALKALLKALKAL 15
|||: | :| |
Db 8 KALKSKLLEVKYL 20

RESULT 3

Matches 6; Conservative 1; Mismatches 3; Indels 1; Gaps 0;

Qy 3 KALKALLKAL 12
|| : || | |
Db 4 KAIAALAKKL 13

RESULT 6
QMVHP2
mastoparan C - European hornet
C;Species: Vespa crabro (European hornet)
C;Date: 28-Feb-1989 #sequence_revision 28-Feb-1989 #text_change 08-Dec-1995
C;Accession: A01779
R;Argiolas, A.; Pisano, J.J.
J. Biol. Chem. 259, 10106-10111, 1984
A;Title: Isolation and characterization of two new peptides, mastoparan C and crabrol
A;Reference number: A92441; MUID:84289390; PMID:6206053
A;Accession: A01779
A;Molecule type: protein
A;Residues: 1-14 <ARG>
C;Comment: This cytoactive peptide from hornet venom induces mast cell degranulation.
C;Superfamily: mastoparan
C;Keywords: amidated carboxyl end; venom
F;14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 47.9%; Score 25; DB 1; Length 14;
Best Local Similarity 54.5%; Pred. No. 5.2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LKALLKALKAL 15
||||| | :
Db 3 LKALLAVAKKI 13

RESULT 7
B33600
glutamate-ammonia ligase (EC 6.3.1.2) - Bradyrhizobium japonicum (fragment)
C;Species: Bradyrhizobium japonicum
C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 15-Jun-2002
C;Accession: B33600
R;Martin, G.B.; Thomashow, M.F.; Chelm, B.K.
J. Bacteriol. 171, 5638-5645, 1989
A;Title: Bradyrhizobium japonicum glnB, a putative nitrogen regulatory gene, is regul
A;Reference number: A33600; MUID:90008805; PMID:2793830
A;Accession: B33600
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-21 <MAR>
A;Cross-references: GB:M26753; NID:g152093; PIDN:AAA26215.1; PID:g152093
C;Keywords: ligase

Query Match 47.9%; Score 25; DB 2; Length 21;
Best Local Similarity 45.5%; Pred. No. 7.8e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KALKALLKALK 13
| | :|| |::
Db 2 KIAKIVLKITK 12

RESULT 8
BMIB
bombinin - Bombina spp.
C;Species: Bombina spp.
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 04-Oct-1990
C;Accession: A01766
R;Csordas, A.; Michl, H.
Monatsh. Chem. 101, 182-189, 1970
A;Title: Isolierung und strukturaufklaerung eines haemolytisch wirksamen polypeptides
A;Reference number: A01766
A;Accession: A01766
A;Molecule type: protein
A;Residues: 1-24 <CSO>

```
A;Note: it is implied that the secretion was collected from more than one species of the
C;Superfamily: melittin major
C;Keywords: amidated carboxyl end
F;24/Modified site: amidated carboxyl end (Asn) #status experimental

  Query Match             37.9%;  Score 25;  DB 1;  Length 24;
  Best Local Similarity   66.7%;  Pred. No. 8.9e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 ALKALLKAL 12
              |||: | | |
Db         10 ALECLAKCL 19


RESULT 9
JN0389
histamine releasing peptide I - oriental hornet
N;Alternate names: venom protein HR 1
C;Species: Vespa orientalis (oriental hornet)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 22-Aug-1997
C;Accession: JN0389; S06445
R;Miroshnikov, A.I.; Snezhkova, I.G.; Marinov, I.V.; Peshekova, O.I.; Rozinov, B.V.; Gus
Bioorg. Khim. 7, 1467-1477, 1981
A;Title: Structure and properties of histamine releasing peptides from the venom of Vesp
A;Reference number: JN0389
A;Accession: JN0389
A;Molecule type: protein
A;Residues: 1-14 <MIR>
R;Dzhibhaev, M.M.; Akhmedova, N.M.; Kazakov, I.; Kornecv, A.F.; Gagel'gans, A.I.
Biochemistry (N.Y.) 53, 183-190, 1988
A;Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis  st
A;Reference number: S06445
A;Accession: S06445
A;Molecule type: protein
A;Residues: 1-14 <IUI>
C;Superfamily: mastoparan
C;Keywords: amidated carboxyl end; venom
F;14/Modified site: amidated carboxyl end (Leu) #status experimental

  Query Match             36.4%;  Score 24;  DB 2;  Length 14;
  Best Local Similarity   62.5%;  Pred. No. 7.6e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 KALKALLK 10
              |: |:|:
Db          4 KAIAAIVK 11


RESULT 10
A44854
L-2,4-diaminobutyrate decarboxylase (EC 4.1.1.-)  Acinetobacter calcoaceticus (fragment
N;Alternate names: DABA decarboxylase
C;Species: Acinetobacter calcoaceticus
C;Date: 23-Mar-1992 #sequence_revision 18-Nov-1994 #text_change 10-Nov-1995
C;Accession: A44854; A41817
R;Yamamoto, S.; Suzuki, Y.; Tougou, K.; Shinoda, S.
J. Gen. Microbiol. 138, 1461-1465, 1992
A;Title: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from A
A;Reference number: A44854; MUID:92381494; PMID:1512577
A;Accession: A44854
A;Molecule type: protein
A;Residues: 1-19 <YAM>
A;Experimental source: ATCC 23055
A;Note: sequence extracted from NCBI backbone (NCBIP:112331)
C;Keywords: carbon-carbon lyase; carboxy-lyase

  Query Match             36.4%;  Score 24;  DB 2;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 1e+03;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FAKALKALL 9
              ||:  |:||
Db          8 FAEHRKALL 16


RESULT 11
B35372
unidentified low M-r protein - Yersinia pseudotuberculosis (fragment)
C;Species: Yersinia pseudotuberculosis
C;Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 19-Apr-1996
C;Accession: B35372
R;Han, O.; Miller, V.P.; Liu, H.
J. Biol. Chem. 265, 8033-8041, 1990
A;Title: Mechanistic studies of the biosynthesis of 3,6-dideoxyhexoses in Yersinia ps
B;dichlorophenolindolphenol oxidoreductase activity.
A;Reference number: A35372; MUID:90244678; PMID:2159466
A;Accession: B35372
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <HAN>

  Query Match             36.4%;  Score 24;  DB 2;  Length 22;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+03;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 ALLKALKALL 15
              |||:| | ||
Db          7 ALVKELAALL 15


RESULT 12
PN0117
hemoglobin alpha chain - red fox (fragment)
C;Species: Vulpes vulpes (red fox)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 19-May-2000
C;Accession: PN0117
R;Sukhomlinov, B.F.; Konoshenko, S.V.
Mol. Biol. (Mosk.) 5, 415-418, 1971
A;Title: Study on N-terminal sequence of the haemoglobin of Vulpes vulpes fox.
A;Reference number: PN0117
A;Accession: PN0117
A;Molecule type: protein
A;Residues: 1-15 <SUK>
C;Superfamily: globin; globin homology
C;Keywords: blood; erythrocyte; heme; heterotetramer; oxygen carrier

  Query Match             34.8%;  Score 24;  DB 2;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 1.2e+03;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 LKALLKALKA 14
              |   :|:|:|
Db          2 LSPAMKAVKA 11


RESULT 13
B36934
orf3 3' of madA - Thiobacillus versutus (fragment)
C;Species: Thiobacillus versutus
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
C;Accession: B36934
R;Huitema, F.; van Beeumen, J.; van Driessche, G.; Duine, J.A.; Canters, G.W.
J. Bacteriol. 175, 6254-6259, 1993
A;Title: Cloning and sequencing of the gene coding for the large subunit of methylami
A;Reference number: A36934; MUID:94012487; PMID:8407797
A;Accession: B36934
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-25 <HUI>
A;Experimental source: ATCC 25364T
A;Note: sequence extracted from NCBI backbone (NCBIN:138060, NCBIP:138062)

  Query Match             34.8%;  Score 24;  DB 2;  Length 25;
  Best Local Similarity   54.5%;  Pred. No. 2e+03;
  Matches    6;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy          1 AKAIKAIKAIKA 14
              | | | | | |
Db         13 AESIEIAAIIA 24


RESULT 14
[illegible] tRNA ligase (EC 6.1.1.20) beta chain - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 03-Jun-2002
C;Accession: [illegible]
R;[illegible]; Bossard, L.; Heinzel, P.
Nucleic Acids Res. 17, 8099, 1989
A;Title: Nucleotide sequence of the Salmonella typhimurium himA gene.
A;Reference number: S09607; MUID:90067874; PMID:2685752
A;Accession: S09607
A;Molecule type: DNA
A;Residues: 1-14 <BOS>
A;Cross-references: EMBL:X14712; NID:g47704; PIDN:CAA32712.1; PID:g809772
C;Genetics:
A;Gene: [illegible]
A;Note: [illegible] catalyzes transfer of activated phenylalanine to phenylalanyl-tRNA
C;Superfamily: phenylalanine tRNA ligase beta chain
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

  Query Match              33.3%;  Score 22;  DB 2;  Length 14;
  Best Local Similarity    50.0%;  Pred. No. 1.2e+03;
  Matches    4;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AKAIKAIKAIKA 14
              | | | | | |
Db          1 AESIEIAAIIAA 12


RESULT 15
S08628
[illegible] 5'-monodeiminase - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Feb-1997 #sequence_revision 14-Mar-1997 #text_change 17-Mar-1999
C;Accession: S08628
R;Thon, L.K.; Wobal, S.S.; Rupler, R.; Morrell, S.; McKenzie, R.A.; Bollester, T.; [illegible]
Arch. Biochem. Biophys. 322, 490-494, 1995
A;Title: Cytochrome P450-catalyzed covalent binding of methoxychlor to rat hepatic, microsomal
A;Reference number: S08628; MUID:96032659; PMID:7574712
A;Accession: S08628
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <BOS>
C;Superfamily: [illegible]; [illegible]; [illegible]

  Query Match              33.3%;  Score 22;  DB 2;  Length 20;
  Best Local Similarity    57.1%;  Pred. No. 2.8e+03;
  Matches    4;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AKAIKAI 7
              |||.|.|
Db          9 AKAVKAA 15


RESULT 16
[illegible]
C;Species: Bacillus [illegible]sporus (fragment)
C;Species: Bacillus [illegible]sporus
C;Date: 28-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
C;Accession: [illegible]
R;[illegible]; [illegible], February 1994
Submitted to EMBL, February 1994
A;Title: [illegible] Phylogenetic diversity in the genus Bacillus and comparative ribosomal RNA
A;Reference number: [illegible]
A;Accession: [illegible]
A;Molecule type: [illegible]
A;Residues: 1-20 <SOB>
C;Keywords: protein biosynthesis; ribosome

  Query Match              33.3%;  Score 22;  DB 2;  Length 20;
  Best Local Similarity    55.6%;  Pred. No. 2.8e+03;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AKAIKAIIK 10
              |||.|.  ||
Db          1 AKSIQIIIK 9


RESULT 17
S68971
hypothetical protein - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Mar-1999
C;Accession: S68971
R;Nikolelt, K.; Rosenstein, R.; Verhelj, E.M.; Goetz, F.
Eur. J. Biochem. 228, 732-738, 1995
A;Title: Comparative biochemical and molecular analysis of the Staphylococcus hyicus
A;Reference number: S68970; MUID:95255279; PMID:7737171
A;Accession: S68971
A;Molecule type: DNA
A;Residues: 1-21 <NIK>
A;Cross-references: EMBL:M90693
A;Note: the authors translated the codon CAA for residue 7 as Gln

  Query Match              33.3%;  Score 22;  DB 2;  Length 21;
  Best Local Similarity    33.3%;  Pred. No. 2.4e+03;
  Matches    5;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 FAKAIKAIIKAIKAI 15
              |.:.:.:.:.||.|
Db          5 FEQLIGSLEKILKEL 19


RESULT 18
B49410
t-complex polypeptide 1 homolog (peak 7 fraction) - rabbit (fragments)
N;Alternate names: chaperonin homolog (peak 7)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 28-Mar-1995
C;Accession: B49410
R;Rommelaere, H.; Van Troys, M.; Gao, Y.; Melki, R.; Cowan, N.J.; Vandekerckhove, J.;
Proc. Natl. Acad. Sci. U.S.A. 90, 11975-11979, 1993
A;Title: Eukaryotic cytosolic chaperonin contains t complex polypeptide 1 and seven r
A;Reference number: A49410; MUID:94089952; PMID:7903459
A;Accession: B49410
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <ROM>
A;Experimental source: reticulocyte

  Query Match              33.3%;  Score 22;  DB 2;  Length 22;
  Best Local Similarity    50.0%;  Pred. No. 2.5e+03;
  Matches    4;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FAKAIKAI 8
              ||:|.:|:
Db         13 FAEAFEAI 20


RESULT 19
B22317
threonine ammonia-lyase (EC 4.3.1.19) - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 21-Jun-2002
C;Accession: B22317
R;Kim, S.S.; Datta, P.
Biochim. Biophys. Acta 706, 27-35, 1982
A;Title: Chemical characterization of biodegradative threonine dehydratases from two
A;Reference number: A90045; MUID:83023208; PMID:6751404
```

A;Accession: B22317
A;Molecule type: protein
A;Residues: 1-24 <KIM>
C;Superfamily: threonine dehydratase
C;Keywords: ammonia-lyase; carbon-nitrogen lyase, carbon-oxygen lyase, hydro-lyase, thr

Query Match 33.3%; Score 22; DB 2; Length 24;
Best Local Similarity 41.7%; Pred. No. 2.7e+03;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 ALKALLKALKAL 15
Db 10 AIK-LLEAKKAL 21

RESULT 20
A41037
antimicrobial peptide PGQ - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 30-Sep-1992
C;Accession: A41037
R;Moore, K.S.; Bevins, C.L.; Brasseur, M.M.; Tomassini, N.; Turner, K.; Eck, H.; Gasla
J. Biol. Chem. 266, 19851-19857, 1991
A;Title: Antimicrobial peptides in the stomach of Xenopus laevis.
A;Reference number: A41037; MUID:92011794; PMID:1717472
A;Accession: A41037
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-24 <MOO>

Query Match 33.3%; Score 22; DB 2; Length 24;
Best Local Similarity 71.4%; Pred. No. 2.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ALKALLK 10
Db 17 ALNAVLK 23

RESULT 21
PQ0683
photosystem I P6,18 P1 chain - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 29-May-1994 #sequence_revision 29-May-1994 #text_change 17-Mar-1999
C;Accession: PQ0683; PQ0670
R;Hoffer, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.
Plant Physiol. 102, 1259-1267, 1993
A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are a
A;Reference number: PQ0667; MUID:94105445; PMID:8278548
A;Accession: PQ0683
A;Molecule type: protein
A;Residues: 1-25 <OBO>
A;Accession: PQ0670
A;Molecule type: protein
A;Residues: 1-16 <OB2>
C;Superfamily: photosystem I chain III
C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 33.3%; Score 22; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 2.8e+03;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 FAKALKALLKAL 12
Db 14 FAKAAKQAAAKL 25

RESULT 22
A45373
amino-acid racemase (EC 5.1.1.10) - Pseudomonas striata (fragment)
N;Alternate names: broad specificity amino acid racemase
N;Contains: alanine racemase (EC 5.1.1.1)
C;Species: Pseudomonas striata
C;Date: 29-Dec-1997 #sequence_revision 29-Dec-1997 #text_change 05-Dec-1998
C;Accession: A29520
R;Roise, D.; Soda, K.; Yagi, T.; Walsh, C.T.
Biochemistry 23, 5195-5201, 1984
A;Title: Inactivation of the Pseudomonas striata broad specificity amino acid racemas
tudies.
A;Reference number: A29520; MUID:85072810; PMID:6439247
A;Accession: A29520
A;Molecule type: protein
A;Residues: 1-16 <ROI>
A;Experimental Source: strain AKU 0813
C;Comment: This broad specificity amino acid racemase has strong alanine racemase (EC
C;Keywords: isomerase; phosphoprotein; pyridoxal phosphate
F;6/binding site - pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 31.8%; Score 21; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 2.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LKALLKA 11
Db 1 LKAVLKA 7

RESULT 23
S21669
1H-4-oxoquinoline monooxygenase - Pseudomonas putida
C;Species: Pseudomonas putida
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S21669
R;Block, D.W.; Lingens, F.
Biol. Chem. Hoppe-Seyler 373, 249-254, 1992
A;Title: Microbial metabolism of quinoline and related compounds. XIII. Purification
A;Reference number: S21669; MUID:92329004; PMID:1627263
A;Accession: S21669
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <BLO>

Query Match 31.8%; Score 21; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AKALKALL 9
Db 1 ANGLKALI 8

RESULT 24
S45373
translation elongation factor EF-1a - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C;Accession: S45373
R;Marty, I.; Bruquidou, C.; Chartier, Y.; Meyer, Y.
Plant J. 4, 265-278, 1993
A;Title: Growth-related gene expression in Nicotiana tabacum mesophyll protoplasts.
A;Reference number: S45372; MUID:94035181; PMID:8220482
A;Accession: S45373
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-18 <MAR>
A;Cross-references: EMBL:Z11080, NID:g443955, PIDN:CAA78458.1; PID:g443956

Query Match 31.8%; Score 21; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 AKALKALLKALK 13
Db 7 AKVLKAAAAKKK 18

RESULT 27
A
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence_revision 09-Mar-1991 #text_change 03-Jun-2002
C;Accession: A45960
R;Gledhill, C.
submitted to the Protein Sequence Database, February 1991
A;Reference number: A45960
A;Accession: A45960
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <GLE>
C;Superfamily: H+-transporting ATP synthase gamma chain
C;Keywords: ATP synthesis; hydrolase; membrane associated complex; mitochondrion; oxi

Query Match 31.8%; Score 21; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 3.3e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AKALKALKALK 12
Db 1 KKLEKLKKLKK 11

RESULT 28
B
C;Species: Homo sapiens (human)
C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 19-Jun-1992
C;Accession: B33290
R;Fiedler, H.; Kraft, R.; Zerial, M.F.
Eur. Mol. Biol. Organ. J. 7, 961-967, 1988
A;Title: Molecular changes associated with induction of cell death in a human T cell leu
A;Reference number: A33290; MUID:89322258; PMID:2546549
A;Accession: B33290
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <BAX>

Query Match 31.8%; Score 21; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 3.3e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KALKALKALK 12
Db 1 KAVIKAIK 10

RESULT 29
A
C;Species: Homo sapiens (human)
C;Date: 01-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 12-Apr-1995
C;Accession: A45918
R;Gilbert, M.M.; Schaffer, M.A.; Kawiswicz, M.A.; Kendrick, N.
submitted to the Protein Sequence Database, February 1995
A;Description: Isolation, characterization and sequence of stone proteins.
A;Reference number: A45918
A;Accession: A45918
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <BIN>

Query Match 31.8%; Score 21; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 3.3e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AKALKALKALKA 13
Db 1 KKLEKLKKLKKA 12

RESULT 28
A45913
plantaricin A - Lactobacillus plantarum
C;Species: Lactobacillus plantarum
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 12-Sep-1997
C;Accession: A45913
R;Nissen-Meyer, J.; Grady Larsen, A.; Clotten, K.; Daeschel, M.; Moe, I.F.
submitted to the Protein Sequence Database, April 1993
A;Reference number: A45913
A;Accession: A45913
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <NIS>
C;Keywords: antibiotic; bacteriocin

Query Match 31.8%; Score 21; DB 2; Length 22;
Best Local Similarity 41.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AKALKALKALK 13
Db 8 AIAIKQVKKLPK 19

RESULT 29
S68391
B+-transporting two-sector ATPase (EC 3.6.3.14) delta chain, chloroplast - Chlamydomo
N;Alternate names: ATP synthase delta chain
C;Species: Chlamydomonas reinhardtii
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 03-Jun-2002
C;Accession: S68391
R;Fiedler, H.K.; Schmid, K.; Leu, S.; Shavit, N.; Strotmann, H.
FEBS Lett. 377, 163-166, 1995
A;Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-termin
A;Reference number: S68388; MUID:96128220; PMID:8543042
A;Accession: S68391
A;Molecule type: protein
A;Residues: 1-24 <FIE>
A;Experimental source: strain CW15
C;Genetics:
A;Genome: nuclear
C;Superfamily: B+-transporting ATP synthase delta chain
C;Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane associated complex; th

Query Match 31.8%; Score 21; DB 2; Length 24;
Best Local Similarity 62.5%; Pred. No. 3.6e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FAKALKAL 8
Db 9 YAKALVEL 16

RESULT 30
H20554
hemocyanin subunit VI - Atlantic horseshoe crab (fragment)
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 08-Jul-1994
C;Accession: H20554
R;Lamy, J.; Lamy, J.; Sizaret, P.Y.; Billiald, P.; Jollès, P.; Jolles, J.; Erlenmann,
Biochemistry 22, 5673-5683, 1983
A;Title: Quaternary structure of Limulus polyphemus hemocyanin.
A;Reference number: A90478
A;Accession: H20554
A;Molecule type: protein
A;Residues: 1-24 <LAM>
C;Comment: Limulus polyphemus hemocyanin is an association of eight different subunit

Query Match 31.8%; Score 21; DB 2; Length 24;
Best Local Similarity 54.5%; Pred. No. 3.6e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LKALLKALKAL 15

```
                    : : | :  : :
Db          2 LGALEKQLRVL 12


RESULT 31
PN0632
biphenyl dioxygenase (EC 1.14.-.-) A4 - Pseudomonas sp. (strain LB400) (fragment)
C;Species: Pseudomonas sp.
C;Date: 30-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 12 Apr-1995
C;Accession: PN0632
R;Hofer, B.; Eltis, L.D.; Dowling, D.N.; Timmis, K.N.
Gene 130, 47-55, 1993
A;Title: Genetic analysis of a Pseudomonas locus encoding a pathway for biphenyl/polychl
A;Reference number: PN0632; MUID:93345022; PMID:8344527
A;Accession: PN0632
A;Molecule type: DNA
A;Residues: 1-25 <HOF>
A;Cross-references: GB:X66122
C;Genetics:
A;Gene: bphA4
C;Superfamily: toluene dioxygenase ferredoxin reductase component
C;Keywords: oxidoreductase; PCB biodegradation

  Query Match             31.8%;  Score 21;  DB 2;  Length 25;
  Best Local Similarity   71.4%;  Pred. No. 4.1e+03;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 LKALLKA 11
              |: ||||
Db         16 LRDLLKA 22


RESULT 32
B69274
hypothetical protein AF0194 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: B69274
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Cocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; Spriggs, T.; Artiach, P.; Faine, B.P.; Sykes, S.
Smith, H.O.; Woose, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: B69274
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-25 <KLE>
A;Cross-references: GB:AE001093; GB:AE000782; NID:g2689416; PIDN:AAB91054.1; PID:g265046

  Query Match             31.8%;  Score 21;  DB 2;  Length 25;
  Best Local Similarity   57.1%;  Pred. No. 4.1e+03;
  Matches    4;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 KALLKAL 12
              :|:||.:
Db          4 KAVLKGM 10


RESULT 33
S29789
hypothetical protein - Thermoplasma acidophilum (fragment)
C;Species: Thermoplasma acidophilum
C;Date: 25-Feb-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C;Accession: S29789
R;Bright, J.R.; Byrom, D.; Danson, M.J.; Hough, D.W.; Towner, P.
Eur. J. Biochem. 211, 549-554, 1993
A;Title: Cloning, sequencing and expression of the gene encoding glucose dehydrogenase f
A;Reference number: S29788; MUID:93170285; PMID:8436115
A;Accession: S29789
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-14 <BRI>
A;Cross-references: EMBL:X59788

  Query Match             30.3%;  Score 20;  DB 2;  Length 14;
  Best Local Similarity   45.5%;  Pred. No. 4.3e+03;
  Matches    5;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 LKALLKALKAL 15
              :| ||| :  |
Db          1 MKDLLKRIDDL 11


RESULT 34
PT0095
H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain, mitochondrial - mouse (f
C;Species: Mus musculus (house mouse)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 03-Jun-2002
C;Accession: PT0095
R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.
submitted to JIPID, July 1998
A;Description: Proteome analysis of mouse brain.
A;Reference number: PT0091
A;Accession: PT0095
A;Molecule type: protein
A;Residues: 1-15 <KAW>
A;Experimental source: brain, striatum
C;Keywords: hydrolase; mitochondrion

  Query Match             30.3%;  Score 20;  DB 2;  Length 15;
  Best Local Similarity   36.4%;  Pred. No. 4.6e+03;
  Matches    4;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 KALKALLKALK 13
              | :   || :|
Db          4 KXIIXPLFXIK 14


RESULT 35
S78767
ribosomal protein MRP-S29, mitochondrial - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 26-Sep-1999 #sequence_revision 26-Sep-1999 #text_change 20-Sep-1999
C;Accession: S78767
R;Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A;Reference number: S78760
A;Accession: S78767
A;Molecule type: protein
A;Residues: 1-18 <GRA>
C;Keywords: mitochondrion
F;1-18/Product: ribosomal protein MRP-S29 (fragment) #status experimental <MAT

  Query Match             30.3%;  Score 20;  DB 2;  Length 18;
  Best Local Similarity   44.4%;  Pred. No. 4.3e+03;
  Matches    4;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 LKALLKALK 13
              |  :|||::
Db          3 LALILKAMQ 11


RESULT 36
B44581
bombinin H Met-8 - yellow-bellied toad
C;Species: Bombina variegata (yellow-bellied toad)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 11 Jan 2000
C;Accession: B44581
R;Mignogna, G.; Simmaco, M.; Kreil, G.; Barra, D.
EMBO J. 12, 4829-4832, 1993
A;Title: Antibacterial and haemolytic peptides containing D-alloisoleucine from the s
A;Reference number: S39612; MUID:94038067; PMID:8223491
A;Accession: B44581
```

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1 <MIT>
C;Superfamily: bombesin H precursor
C;Keywords: amidated carboxyl end; D-amino acid
F;2/Modified site: D-allo-isoleucine (Ile) #status experimental
F;2/Modified site: amidated carboxyl end (Ile) #status predicted

Query Match 80.4%; Score 20; DB 2; Length 20;
Best Local Similarity 55.6%; Pred. No. 4.8e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AKALKALKAL 10
Db 11 AIIIIKKI 20

RESULT 37
A31944
tRNA ligase (EC 6.1.1.19) - rat (fragment)
N;Species: Rattus norvegicus (Norway rat)
C;Date: 2-Jul-1990 #sequence_revision 12-Oct-1990 #text_change 03-Jun-2002
C;Accession: A31944
R;Lapetina, E.; Beuttenmuller, M.P.
Proc. Natl. Acad. Sci. U.S.A. 87, 8665-8669, 1990
A;Title: Existence of two forms of rat liver arginyl-tRNA synthetase suggests channeling
A;Reference number: A90945; MUID:90525617; PMID:2187187
A;Accession: A31944
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1 <SIV>
C;Keywords: arginyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 80.4%; Score 20; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 4.8e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AKALKA 7
Db 11 EGKAIKA 16

RESULT 38
A27945
P-450 surface antigen - Mycobacterium avium (fragment)
C;Species: Mycobacterium avium
C;Date: 1-Dec-1991 #sequence_revision 31-Dec-1992 #text_change 12-Sep-1997
C;Accession: A27945
R;Fujiwara, H.; Tsuda, K.; Matsuo, S.A.; Catanzaro, A.
Submitted to the Protein Sequence Database, October 1992
A;Reference number: A27945
A;Accession: A27945
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1 <FAV>
A;Note: the authors stated the species as Mycobacterium avium Mycobacterium intracellular
C;Superfamily: Superoxide dismutase
C;Keywords: surface antigen

Query Match 80.4%; Score 20; DB 2; Length 22;
Best Local Similarity 48.0%; Pred. No. 5.2e+03;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 5 KALKALKALKAL 15
Db 4 RAPKIRELNAL 21

RESULT 39
A27945
P-450 - Chinese hamster (fragment)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 1-Dec-1991 #sequence_revision 06-May-1995 #text_change 17-Mar-1999

C;Accession: S43769
R;Zastawny, R.L.; Ling, V.
Biochim. Biophys. Acta 1174, 408-413, 1993
A;Title: Structural and functional analysis of 5' flanking and intron 1 sequences of
A;Reference number: S43768; MUID:93305724; PMID:8100449
A;Accession: S43769
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-22 <ZAS>
A;Cross-references: EMBL:L03287
C;Keywords: glycoprotein

Query Match 80.4%; Score 20; DB 2; Length 22;
Best Local Similarity 55.6%; Pred. No. 5.2e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AKALKALLK 10
Db 9 AKADKGLLE 17

RESULT 40
A31944
cytochrome P450NMa - rabbit (fragment)
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: cryptolagus cuniculus (domestic rabbit)
C;Date: 01-Mar-1990 #sequence_revision 01-Mar-1990 #text_change 05-Mar-1999
C;Accession: A31944
R;Ding, X.; Coon, M.J.
Biochemistry 27, 8330-8337, 1988
A;Title: Purification and characterization of two unique forms of cytochrome P-450 fr
A;Reference number: A90941; MUID:89207441; PMID:3242590
A;Accession: A31944
A;Molecule type: protein
A;Residues: 1-23 <DIN>
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane pro

Query Match 80.4%; Score 20; DB 2; Length 23;
Best Local Similarity 45.5%; Pred. No. 5.5e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LKALLKALKAL 15
Db 8 LAALLASLIVM 18

RESULT 41
S44739
trans-cinnamate 4-monooxygenase (EC 1.14.13.11) - kidney bean (fragment)
N;Alternate name: trans-cinnamic acid hydroxylase
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 05-Mar-1999
C;Accession: S44739
R;Rodgers, M.W.; Zimmerlin, A.; Werck-Reichhart, D.; Bolwell, G.P.
Arch. Biochem. Biophys. 404, 74-80, 1993
A;Title: Microsomally associated heme proteins from French bean: characterization of
A;Reference number: S44739; MUID:93312024; PMID:8323300
A;Accession: S44739
A;Molecule type: protein
A;Residues: 1-23 <ROD>
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: heme; oxidoreductase

Query Match 80.4%; Score 20; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 5.5e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 KALKALLKAL 12
Db 8 KILVALFAAI 17

```
RESULT 42
G20554
hemocyanin subunit V - Atlantic horseshoe crab (fragment)
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 08-Jul-1994
C;Accession: G20554
R;Lamy, J.; Lamy, J.; Sizaret, P.Y.; Billiald, P.; Jolles, P.; Jolles, J.; Feldmann, R.J
Biochemistry 22, 5573-5583, 1983
A;Title: Quaternary structure of Limulus polyphemus hemocyanin.
A;Reference number: A90478
A;Accession: G20554
A;Molecule type: protein
A;Residues: 1-24 <LAM>
C;Comment: Limulus polyphemus hemocyanin is an association of eight different subunits w

  Query Match             30.8%;  Score 20;  DB 2;  Length 24;
  Best Local Similarity   45.5%;  Pred. No. 5.7e+03;
  Matches    5;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 LKALKALKAL 15
              | : | | : :
Db          2 LSVLQKQLKV 12


RESULT 43
B64710
hypothetical protein HP1528 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: B64710
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Lottus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.  Glodek, A.; McKenne
son, K.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: B64710
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-25 <TOM>
A;Cross-references: GB:AE000651; GB:AE000511; NID:g2314708; PIDN:AAD08577.1; PID:g231471

  Query Match             30.8%;  Score 20;  DB 2;  Length 25;
  Best Local Similarity   40.0%;  Pred. No. 5.9e+03;
  Matches    4;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          6 KALKALKAL 15
              | |:| : |
Db         16 KGLVKVNRL 25


RESULT 44
PN0118
hemoglobin beta chain - red fox (fragment)
C;Species: Vulpes vulpes (red fox)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 19-May-2000
C;Accession: PN0118
R;Sokhominov, B.F.; Konoshenko, S.V.
Mol. Biol. (Mosk.) 5, 415-418, 1971
A;Title: Study on N-terminal sequence of the haemoglobin of Vulpes vulpes fox.
A;Reference number: PN0117
A;Accession: PN0118
A;Molecule type: protein
A;Residues: 1-15 <SOK>
C;Superfamily: globin; globin homology
C;Keywords: blood; erythrocyte; heme; heterotetramer; oxygen carrier

  Query Match             29.5%;  Score 19.5;  DB 2;  Length 15;
  Best Local Similarity   66.7%;  Pred. No. 4.3e+03;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          5 LKALLK ALKAL 15
                |||  | |:|||
Db          3 LKAEEPAVKAL 14


RESULT 45
A38841
rhodopsin homolog - squid (Watasenia scintillans) (fragment)
N;Alternate names: visual pigment protein
C;Species: Watasenia scintillans (sparkling enope)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Oct-1992
C;Accession: A38841
R;Seidou, M.; Kubota, I.; Hiraki, K.; Kito, Y.
Biochim. Biophys. Acta 957, 318-321, 1988
A;Title: Amino acid sequence of the retinal binding site of squid visual pigment.
A;Reference number: PF0063; MUID:89051045; PMID:3191148
A;Accession: A38841
A;Molecule type: protein
A;Residues: 1-11 <SEI>
C;Superfamily: vertebrate rhodopsin
C;Keywords: chromoprotein; retinal
F;3/Binding site: retinal (Lys) (covalent) #status experimental

  Query Match             28.8%;  Score 19;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KAKA 4
              ||||
Db          1 KAKA 4


Search completed: August 21, 2003, 08:22:01
Job time : 42 secs
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GenCore version 5.1.6

SW protein protein search, using sw model

Run on: August 21, 2003, 08:19:10 ; Search time 55 Seconds
(without alignments)
85.990 Million cell updates/sec

Title: US-09-820-053A-43
Perfect score: 66
Sequence: 1 FAKALKALLKALKAL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 49179 seqs, 13199718 residues

Total number of hits satisfying chosen parameters: 111939

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep:*
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4: /cgn2_6/ptodata/2/pubaa/US08_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubaa/US09S_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubaa/US09_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubaa/US10_PUBCOMB.pep:*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	66	100.0	15	11	US-09-820-053A-43	Sequence 43, Appl
2	66	100.0	15	15	US-10-109-171-43	Sequence 43, Appl
3	64	97.0	15	11	US-09-820-053A-152	Sequence 152, App
4	64	97.0	15	15	US-10-109-171-152	Sequence 152, App
5	48	72.7	25	11	US-09-820-053A-1	Sequence 1, Appli
6	48	72.7	23	11	US-09-820-053A-2	Sequence 2, Appli
7	48	72.7	23	15	US-10-109-171-1	Sequence 1, Appli
8	48	72.7	23	15	US-10-109-171-2	Sequence 2, Appli
9	43	65.2	23	11	US-09-820-053A-9	Sequence 9, Appli
10	43	65.2	23	11	US-09-820-053A-19	Sequence 19, Appl
11	43	65.2	23	15	US-10-109-171-9	Sequence 9, Appli
12	43	65.2	23	15	US-10-109-171-19	Sequence 19, Appl
13	42	63.6	19	11	US-09-820-053A-12	Sequence 12, Appl
14	42	63.6	19	11	US-09-820-053A-13	Sequence 13, Appl
15	42	63.6	19	15	US-10-109-171-12	Sequence 12, Appl
16	42	63.6	19	15	US-10-109-171-13	Sequence 13, Appl
17	42	63.6	20	11	US-09-820-053A-68	Sequence 68, Appl
18	42	63.6	20	15	US-10-109-171-68	Sequence 68, Appl
19	42	63.6	23	11	US-09-820-053A-15	Sequence 15, Appl
20	42	63.6	23	11	US-09-820-053A-158	Sequence 158, App
21	42	63.6	23	11	US-09-820-053A-159	Sequence 159, App
22	42	63.6	23	15	US-10-109-171-15	Sequence 15, Appl
23	42	63.6	23	15	US-10-109-171-158	Sequence 158, App
24	42	63.6	23	15	US-10-109-171-159	Sequence 159, App
25	41	62.1	15	11	US-09-820-053A-22	Sequence 22, Appl
26	41	62.1	15	15	US-10-109-171-22	Sequence 22, Appl
27	41	62.1	16	11	US-09-820-053A-16	Sequence 16, Appl
28	41	62.1	16	15	US-10-109-171-16	Sequence 16, Appl
29	41	62.1	23	11	US-09-820-053A-161	Sequence 161, App
30	41	62.1	23	15	US-10-109-171-161	Sequence 161, App
31	40	60.6	12	11	US-09-820-053A-106	Sequence 106, App
32	40	60.6	12	15	US-10-109-171-106	Sequence 106, App
33	40	60.6	24	11	US-09-820-053A-8	Sequence 8, Appli
34	40	60.6	24	15	US-10-109-171-8	Sequence 8, Appli
35	40	60.6	25	9	US-09-864-761-34307	Sequence 34307, A
36	39	59.1	21	12	US-09-798-826B-17	Sequence 17, Appl
37	38	57.6	21	11	US-09-820-053A-1	Sequence 1, Appli
38	38	57.6	23	11	US-09-820-053A-10	Sequence 10, Appl
39	38	57.6	23	15	US-10-109-171-10	Sequence 10, Appl
40	37	56.1	17	11	US-09-820-053A-112	Sequence 112, App
41	37	56.1	17	11	US-09-820-053A-115	Sequence 115, App
42	37	56.1	17	15	US-10-109-171-112	Sequence 112, App
43	37	56.1	17	15	US-10-109-171-115	Sequence 115, App
44	37	56.1	18	10	US-09-765-614B-12	Sequence 12, Appl
45	37	56.1	18	10	US-09-925-715-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-820-053A-43
; Sequence 43, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: DEL/027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 43
; LENGTH: 15
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MET-PES
; LOCATION: (1)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-43

Query Match 100.0%; Score 66; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. ...;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAKALKALLKALKAL 15
||||||||||||||| |
Db 1 FAKALKALLKALKAL 15

RESULT 2
US-10-109-171-43
; Sequence 43, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.

; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX.2a
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 15
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (15)
; OTHER INFORMATION: AMIDATION

Query Match 100.0%; Score 60; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AKALKALKALKAL 15
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Db 2 AKALKALKALKAL 15

RESULT 5
US-09-820-053A-1
; Sequence 1, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-09-820-053A-1

Query Match 72.7%; Score 48; DB 11; Length 23;
Best Local Similarity 80.0%; Pred. No. 0.35;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FAKALKALKALKAL 15
|| ||||| |||| |
Db 1 FALALKALKFALKEL 15

RESULT 6
US-09-820-053A-2
; Sequence 2, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (23)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-2

Query Match 72.7%; Score 48; DB 11; Length 23;
Best Local Similarity 80.0%; Pred. No. 0.35;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 FAKALKALLKALKAL 15
              || |||| | ||| |
Db          1 FALALKALEKALEKL 15


RESULT 7
US-10-109-171-1
; Sequence 1, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
;  FILE REFERENCE: HELX028
;  CURRENT APPLICATION NUMBER: US/10/109,171
;  CURRENT FILING DATE:  2002-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;  LENGTH: 23
;  TYPE: PRT
;  ORGANISM: ARTIFICIAL SEQUENCE
;  FEATURE:
;  OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-1

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  Matches   12;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    2;

Qy          1 FAKALKALLKALKAL 15
              || |||| | ||| |
Db          1 FALALKALEKALEKL 15


RESULT 8
US-10-109-171-2
; Sequence 2, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
;  FILE REFERENCE: HELX028
;  CURRENT APPLICATION NUMBER: US/10/109,171
;  CURRENT FILING DATE:  2002-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;  LENGTH: 23
;  TYPE: PRT
;  ORGANISM: ARTIFICIAL SEQUENCE
;  FEATURE:
;  OTHER INFORMATION: SYNTHETIC SEQUENCE
;  NAME/KEY: MOD_RES
;  LOCATION: (23)
;  OTHER INFORMATION: AMIDATION
US-10-109-171-2

  Query Match             72.7%;  Score 48;  DB 15;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 0.35;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |||| |||| |
Db          1 FALALKALKKALKKL 15


RESULT 9
US-09-820-053A-9
; Sequence 9, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
;  FILE REFERENCE: HELX027
;  CURRENT APPLICATION NUMBER: US/09/820,053A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;  LENGTH: 23
;  TYPE: PRT
;  ORGANISM: ARTIFICIAL SEQUENCE
;  FEATURE:
;  OTHER INFORMATION: SYNTHETIC SEQUENCE
;  NAME/KEY: MOD_RES
;  LOCATION: (23)
;  OTHER INFORMATION: AMIDATION
US-09-820-053A-9

  Query Match             65.2%;  Score 43;  DB 11;  Length 23;
  Best Local Similarity   73.3%;  Pred. No. 2;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |||| | || |
Db          1 FALALEALEELEEL 15


RESULT 10
US-09-820-053A-19
; Sequence 19, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
;  FILE REFERENCE: HELX027
;  CURRENT APPLICATION NUMBER: US/09/820,053A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;  LENGTH: 23
;  TYPE: PRT
;  ORGANISM: ARTIFICIAL SEQUENCE
;  FEATURE:
;  OTHER INFORMATION: SYNTHETIC SEQUENCE
;  NAME/KEY: MOD_RES
;  LOCATION: (13)..(14)
;  OTHER INFORMATION: Xaa = D-lysine
US-09-820-053A-19

  Query Match             65.2%;  Score 43;  DB 11;  Length 23;
  Best Local Similarity   73.3%;  Pred. No. 2;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |||| ||| |
Db          1 FALALEALEEALXXL 15


RESULT 11
US-10-109-171-9
; Sequence 9, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
;  FILE REFERENCE: HELX028
;  CURRENT APPLICATION NUMBER: US/10/109,171
;  CURRENT FILING DATE:  2002-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;  LENGTH: 23
;  TYPE: PRT
;  ORGANISM: ARTIFICIAL SEQUENCE
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    NAME/KEY: MOD_RES
    LOCATION: (19)
    OTHER INFORMATION: AMIDATION
US-09-820-053A-43

  Query Match             63.6%;  Score 42;  DB 15;  Length 23;
  Best Local Similarity   73.3%;  Pred. No. 2;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              :  :  :  :  :  :
Db          1 FAKALKALEKLEKAL 15


RESULT 14
US-09-820-053A-13
; Sequence 13, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
;  FILE REFERENCE: HELX027
;  CURRENT APPLICATION NUMBER: US/09/820,053A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
;  LENGTH: 19
;  TYPE: PRT
;  ORGANISM: ARTIFICIAL SEQUENCE
;  FEATURE:
;  OTHER INFORMATION: SYNTHETIC SEQUENCE
US-09-820-053A-13

  Query Match             63.6%;  Score 42;  DB 11;  Length 19;
  Best Local Similarity   73.3%;  Pred. No. 2.4;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              :  :  :  :  :  :
Db          1 FALALKALEKLEKAL 15


RESULT 15
US-10-109-171-12
; Sequence 12, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
;  FILE REFERENCE: HELX028
;  CURRENT APPLICATION NUMBER: US/10/109,171
;  CURRENT FILING DATE:  2002-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
;  LENGTH: 19
;  TYPE: PRT
;  ORGANISM: ARTIFICIAL SEQUENCE
;  FEATURE:
;  OTHER INFORMATION: SYNTHETIC SEQUENCE
;  NAME/KEY: MOD_RES
;  LOCATION: (19)
;  OTHER INFORMATION: AMIDATION
US-10-109-171-12

  Query Match             63.6%;  Score 42;  DB 15;  Length 19;
  Best Local Similarity   73.3%;  Pred. No. 2.4;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              :  :  :  :  :  :
Db          1 FALALKALEKLEKAL 15


RESULT 16
US-10-109-171-13
; Sequence 13, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
;  FILE REFERENCE: HELX027
;  CURRENT APPLICATION NUMBER: US/10/109,171
;  CURRENT FILING DATE:  2002-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;    LENGTH: 19
;    TYPE: PRT
;    ORGANISM: ARTIFICIAL SEQUENCE
;    FEATURE:
;    OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-13

  Query Match             63.6%;  Score 42;  DB 15;  Length 19;
  Best Local Similarity   73.3%;  Pred. No. 2.4;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || |||| | |||
Db          1 FALALKALKKLKKAL 15


RESULT 17
US-09-820-053A-68
; Sequence 68, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
;  FILE REFERENCE: HELX027
;  CURRENT APPLICATION NUMBER: US/09/820,053A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
;    LENGTH: 20
;    TYPE: PRT
;    ORGANISM: ARTIFICIAL SEQUENCE
;    FEATURE:
;    OTHER INFORMATION: SYNTHETIC SEQUENCE
;    NAME/KEY: MOD_RES
;    LOCATION: (20)
;    OTHER INFORMATION: AMIDATION
US-09-820-053A-68

  Query Match             63.6%;  Score 42;  DB 11;  Length 20;
  Best Local Similarity   76.9%;  Pred. No. 2.5;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALK 13
              | |||| | ||||
Db          5 FEKALEELEKALF 17


RESULT 18
US-10-109-171-68
; Sequence 68, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
;  FILE REFERENCE: HELX028
;  CURRENT APPLICATION NUMBER: US/10/109,171
;  CURRENT FILING DATE:  2002-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
;    LENGTH: 20
;    TYPE: PRT
;    ORGANISM: ARTIFICIAL SEQUENCE
;    FEATURE:
;    OTHER INFORMATION: SYNTHETIC SEQUENCE
;    NAME/KEY: MOD_RES
;    LOCATION: (20)
;    OTHER INFORMATION: AMIDATION
US-10-109-171-68

  Query Match             63.6%;  Score 42;  DB 15;  Length 20;
  Best Local Similarity   76.9%;  Pred. No. 2.5;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALK 13
              | |||| | ||||
Db          5 FEKALEELEKALF 17


RESULT 19
US-09-820-053A-15
; Sequence 15, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
;  FILE REFERENCE: HELX027
;  CURRENT APPLICATION NUMBER: US/09/820,053A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;    LENGTH: 23
;    TYPE: PRT
;    ORGANISM: ARTIFICIAL SEQUENCE
;    FEATURE:
;    OTHER INFORMATION: SYNTHETIC SEQUENCE
;    NAME/KEY: MOD_RES
;    LOCATION: (23)
;    OTHER INFORMATION: AMIDATION
US-09-820-053A-15

  Query Match             63.6%;  Score 42;  DB 11;  Length 23;
  Best Local Similarity   78.6%;  Pred. No. 2.9;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              | ||||| |||| |
Db          2 ALALKALKKALKKL 15


RESULT 20
US-09-820-053A-158
; Sequence 158, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
;  FILE REFERENCE: HELX027
;  CURRENT APPLICATION NUMBER: US/09/820,053A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 158
;    LENGTH: 23
;    TYPE: PRT
;    ORGANISM: ARTIFICIAL SEQUENCE
;    FEATURE:
;    OTHER INFORMATION: SYNTHETIC SEQUENCE
;    NAME/KEY: MOD_RES
;    LOCATION: (23)
;    OTHER INFORMATION: AMIDATION
US-09-820-053A-158

  Query Match             63.6%;  Score 42;  DB 11;  Length 23;
  Best Local Similarity   78.6%;  Pred. No. 2.9;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy          2 AKALKALKALKAL 15
              | |||| |||| |
Db          2 ALALKALKKALKKL 15


RESULT 23
; Sequence 23, Application US/09820053A
; Publication No. US2003008243A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
;  FILE REFERENCE: BELX027
;  CURRENT APPLICATION NUMBER: US/09/820,053A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;  LENGTH: 23
;  TYPE: PRT
;  ORGANISM: ARTIFICIAL SEQUENCE
;  FEATURE:
;  OTHER INFORMATION: SYNTHETIC SEQUENCE
;  NAME/KEY: MISC_FEA
;  LOCATION: (23)
;  OTHER INFORMATION: AMIDATION
US 10-109-171 23

  Query Match             63.6%;  Score 42;  DB 11;  Length 23;
  Best Local Similarity   78.6%;  Pred. No. 2.9;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AKALKALKALKAL 15
              | |||| |||| |
Db          2 ALALKALKKALKKL 15


RESULT 24
US 10-109-171-159
; Sequence 159, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
;  FILE REFERENCE: BELX028
;  CURRENT APPLICATION NUMBER: US/10/109,171
;  CURRENT FILING DATE:  2002-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
;  LENGTH: 23
;  TYPE: PRT
;  ORGANISM: ARTIFICIAL SEQUENCE
;  FEATURE:
;  OTHER INFORMATION: SYNTHETIC SEQUENCE
US 10-109-171-159

  Query Match             63.6%;  Score 42;  DB 15;  Length 23;
  Best Local Similarity   78.6%;  Pred. No. 2.9;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AKALKALKALKAL 15
              | |||| |||| |
Db          2 ALALKALKKALKKL 15


RESULT 25
US-09-820-053A-22
; Sequence 22, Application US/09820053A
; Publication No. US20030082434A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
;  FILE REFERENCE: BELX027
;  CURRENT APPLICATION NUMBER: US/09/820,053A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;  LENGTH: 15
;  TYPE: PRT
;  ORGANISM: ARTIFICIAL SEQUENCE
;  FEATURE:
;  OTHER INFORMATION: SYNTHETIC SEQUENCE
```

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;   NAME/KEY: MOD_RES
;   LOCATION: (15)
;   OTHER INFORMATION: AMIDATION
US-09-820-053A-22

  Query Match             62.1%;  Score 41;  DB 11;  Length 15;
  Best Local Similarity   73.3%;  Pred. No. 2.6;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              | | | || | | |||
Db          1 FALAKKALKKAKKAL 15


RESULT 26
US-10-109-171-22
; Sequence 22, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
;  FILE REFERENCE: HELX028
;  CURRENT APPLICATION NUMBER: US/10/109,171
;  CURRENT FILING DATE:  2002-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC SEQUENCE
;   NAME/KEY: MOD_RES
;   LOCATION: (15)
;   OTHER INFORMATION: AMIDATION
US-10-109-171-22

  Query Match             62.1%;  Score 41;  DB 15;  Length 15;
  Best Local Similarity   73.3%;  Pred. No. 2.6;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 FAKALKA..KALKAL 15
              | | | |. | | |||
Db          1 FALAKKA.FKAKKAL 15


RESULT 27
US-09-820-053A-16
; Sequence 16, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
;  FILE REFERENCE: HELX027
;  CURRENT APPLICATION NUMBER: US/09/820,053A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC SEQUENCE
;   NAME/KEY: MOD_RES
;   LOCATION: (16)
;   OTHER INFORMATION: AMIDATION
US-09-820-053A-16

  Query Match             62.1%;  Score 41;  DB 11;  Length 16;
  Best Local Similarity   76.9%;  Pred. No. 2.8;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||| |  |||||
Db          1 FALAKKALKKALKAL 15


RESULT 28
US-10-109-171-16
; Sequence 16, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
;  FILE REFERENCE: HELX028
;  CURRENT APPLICATION NUMBER: US/10/109,171
;  CURRENT FILING DATE:  2002-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC SEQUENCE
;   NAME/KEY: MOD_RES
;   LOCATION: (16)
;   OTHER INFORMATION: AMIDATION
US-10-109-171-16

  Query Match             62.1%;  Score 41;  DB 15;  Length 16;
  Best Local Similarity   76.9%;  Pred. No. 2.8;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 FAKALKALLKALKAL 15
              || ||| |  |||||
Db          1 FALALKKALKALKAL 15


RESULT 29
US-09-820-053A-161
; Sequence 161, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
;  FILE REFERENCE: HELX027
;  CURRENT APPLICATION NUMBER: US/09/820,053A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 161
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC SEQUENCE
;   NAME/KEY: MOD_RES
;   LOCATION: (23)
;   OTHER INFORMATION: AMIDATION
US-09-820-053A-161

  Query Match             62.1%;  Score 41;  DB 11;  Length 23;
  Best Local Similarity   76.9%;  Pred. No. 4.1;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 KALKALLKALKAL 15
              |||| ||| || |
Db          6 KALKKLLKKLKKL 18


RESULT 30
US-10-109-171-161
; Sequence 161, Application US/10109171
; Publication No. US20030109452A1
```

; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (23)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-23

Query Match 60.6%; Score 40; DB 15; Length 23;
Best Local Similarity 83.3%; Pred. No. 4.1;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KALKALKALKAL 12
|| | |||| ||
Db 1 KALKKLKKLKKL 12

RESULT 33
US-09-820-053A-8
; Sequence 8, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (23)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-8

Query Match 60.6%; Score 40; DB 11; Length 23;
Best Local Similarity 71.4%; Pred. No. 5.9;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AKALKALKALKAL 15
|:|| | | || |
Db 5 AKALKKLAKKLKKL 18

RESULT 34
US-10-109-171-8
; Sequence 8, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (23)
; OTHER INFORMATION: AMIDATION
US-10-109-171-8

; LENGTH: 12
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: AMIDATION
US-10-109-171-106

Query Match 60.6%; Score 40; DB 15; Length 12;
Best Local Similarity 83.3%; Pred. No. 3;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KALKALKALKAL 12
|| | |||| ||
Db 1 KALKKLKKLKKL 12

```
  Query Match             60.6%;  Score 40;  DB 15;  Length 23;
  Best Local Similarity   71.4%;  Pred. No. 5.9;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              ||:||: | :|| |
Db          5 AKALRSLAKKIKAL 18


RESULT 35
US-09-864-761-34307
; Sequence 34307, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Banzol, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Agouron X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,356
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,966
;  PRIOR FILING DATE: 2000-08-04
;  PRIOR APPLICATION NUMBER: GB 0026316.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,759
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34307
;   LENGTH: 25
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AF009269.1
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL =  12
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL =  76
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL =  26
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL =  49
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL =  48
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL =  18
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL =  85
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL =  26
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL =  17
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL =  40
;   OTHER INFORMATION: SWISSPROT HIT: Q95281, EVALUE 5.00e-06
;   OTHER INFORMATION: EST_HUMAN HIT: BE880966.1, EVALUE 7.00e-05
US-09-864-761-34307

  Query Match             60.6%;  Score 40;  DB 9;  Length 25;
  Best Local Similarity   64.3%;  Pred. No. 6.4;
  Matches    9;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AKALKALLKALKAL 15
              |||: |  ||:|||
Db          7 AKAMSARAKAIKAL 20


RESULT 36
US-09-798-026B-17
; Sequence 17, Application US/09798026B
; Publication No. US20030148936A1
; GENERAL INFORMATION:
;  APPLICANT: ALPHARMA AS
;  TITLE OF INVENTION: Cytotoxic Peptides Modified by Bulky or Lipophilic Moieties
;  FILE REFERENCE: 40745-2
;  CURRENT APPLICATION NUMBER: US/09/798,026B
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER: GB 9818938.4
;  PRIOR FILING DATE: 1998-08-28
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(21)
;   OTHER INFORMATION: Artificial peptide - native MSI20 peptide or mutated native MS
;   OTHER INFORMATION: peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (6)..(6)
;   OTHER INFORMATION: Replacement possible substitution (A-W)
US-09-798-026B-17

  Query Match             59.1%;  Score 39;  DB 12;  Length 21;
  Best Local Similarity   91.8%;  Pred. No. 7.6;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 KALKALLKALKAL 15
              |||| ||||| |
Db          5 KALKVALKALK 15


RESULT 37
US-09-876-904A-1
; Sequence 1, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
;  APPLICANT: BOULIKAS, TENI
;  TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
;  TITLE OF INVENTION:  AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
;  TITLE OF INVENTION:  CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
;  FILE REFERENCE: TB-2002.00
;  CURRENT APPLICATION NUMBER: US/09/876,904A
;  CURRENT FILING DATE:  2001-06-08
;  PRIOR APPLICATION NUMBER: US 60/210,625
;  PRIOR FILING DATE: 2000-06-09
;  NUMBER OF SEQ ID NOS: 629
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
```

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;  LENGTH: 23
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Pseudomonic/NLS peptide
;  NAME/KEY: MOD_RES
;  LOCATION: (23)
;  OTHER INFORMATION: AMIDATION
US  09-820-053A-1

  Query Match             33.3%;  Score 38;  DB 11;  Length 23;
  Best Local Similarity   66.7%;  Pred. No. 12;
  Matches   10;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 FAKALKALKALKAL 15
              |||||||||||||||
Db          9 FAKALKALKALKAL 23


RESULT 39
US 09-820-053A-108
; Sequence 108, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
;  FILE REFERENCE: HELX027
;  CURRENT APPLICATION NUMBER: US/09/820,053A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
;  LENGTH: 14
;  TYPE: PRT
;  ORGANISM: ARTIFICIAL SEQUENCE
;  FEATURE:
;  OTHER INFORMATION: SYNTHETIC SEQUENCE
;  NAME/KEY: MOD_RES
;  LOCATION: (14)
;  OTHER INFORMATION: AMIDATION
US 09-820-053A-108

  Query Match             56.1%;  Score 47;  DB 11;  Length 14;
  Best Local Similarity   81.8%;  Pred. No. 1.2;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 KALKALKALKALKA 16
              ||| |||||||||
Db          1 KALKALKALKALKA 14


RESULT 40
US 09-820-053A-112
; Sequence 112, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
;  FILE REFERENCE: HELX027
;  CURRENT APPLICATION NUMBER: US/09/820,053A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
;  LENGTH: 17
;  TYPE: PRT
;  ORGANISM: ARTIFICIAL SEQUENCE
;  FEATURE:
;  OTHER INFORMATION: SYNTHETIC SEQUENCE
;  NAME/KEY: MOD_RES
;  LOCATION: (17)
;  OTHER INFORMATION: AMIDATION
US 09-820-053A-112

  Query Match             56.1%;  Score 47;  DB 11;  Length 17;
  Best Local Similarity   81.8%;  Pred. No. 1.2;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ALKALKALKALKA 14
              ||| |||||||||
Db          3 ALKALKALKALKA 13


RESULT 41
US 09-820-053A-115
; Sequence 115, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
;  FILE REFERENCE: HELX027
;  CURRENT APPLICATION NUMBER: US/09/820,053A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
;  LENGTH: 17
;  TYPE: PRT
;  ORGANISM: ARTIFICIAL SEQUENCE
;  FEATURE:
;  OTHER INFORMATION: SYNTHETIC SEQUENCE
;  NAME/KEY: MOD_RES
;  LOCATION: (17)
;  OTHER INFORMATION: AMIDATION
US 09-820-053A-115

  Query Match             56.1%;  Score 47;  DB 11;  Length 17;
  Best Local Similarity   81.8%;  Pred. No. 1.2;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 KALKALKALKALK 15
              |||| |||||||||
Db          4 KALKKLKKALKALK 14


RESULT 42
```

```
US-10-109-171-112
; Sequence 112, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
;  FILE REFERENCE: HELX028
;  CURRENT APPLICATION NUMBER: US/10/109,171
;  CURRENT FILING DATE:  2002-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC SEQUENCE
;   NAME/KEY: MOD_RES
;   LOCATION: (17)
;   OTHER INFORMATION: AMIDATION
US-10-109-171-112

  Query Match             56.1%;  Score 37;  DB 15;  Length 17;
  Best Local Similarity   81.8%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 AlKAlLkAlKA 14
              ||| | |||| |
Db          3 ALKLALKALKA 13


RESULT 43
US-10-109-171-115
; Sequence 115, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
;  FILE REFERENCE: HELX028
;  CURRENT APPLICATION NUMBER: US/10/109,171
;  CURRENT FILING DATE:  2002-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC SEQUENCE
;   NAME/KEY: MOD_RES
;   LOCATION: (17)
;   OTHER INFORMATION: AMIDATION
US-10-109-171-115

  Query Match             56.1%;  Score 37;  DB 15;  Length 17;
  Best Local Similarity   81.8%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 KALKALLKALK 13
              ||| | | | |
Db          4 KSLRSLFRSLK 14


RESULT 44
US-09-765-614B-12
; Sequence 12, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
;  APPLICANT: Nycomed Imaging AS
;  TITLE OF INVENTION: Improvements in or relating to
;  TITLE OF INVENTION:  diagnostic/therapeutic
;  TITLE OF INVENTION:  agents
;  FILE REFERENCE: PPS/Klarchess/054
;  CURRENT APPLICATION NUMBER: US/09/765,614B
;  CURRENT FILING DATE:  2001-07-10
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial
;   OTHER INFORMATION: Sequence:Endothelial
;   OTHER INFORMATION: cell binding lipopeptide
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: 2-n-hexadecylstearyl Lys
;   NAME/KEY: MOD_RES
;   LOCATION: (18)
;   OTHER INFORMATION: AMIDATION
US-09-765-614B-12

  Query Match             56.1%;  Score 37;  DB 10;  Length 18;
  Best Local Similarity   81.8%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 AlKAlLkAlKA 14
              ||| | |||| |
Db          3 ALKLALKALKA 13


RESULT 45
US-09-925-715-12
; Sequence 12, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
;  APPLICANT: Nycomed Imaging AS
;  TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
;  TITLE OF INVENTION:  agents
;  FILE REFERENCE: PPS/Klarchess/226
;  CURRENT APPLICATION NUMBER: US/09/925,715
;  CURRENT FILING DATE:  2001-08-10
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Synthetic
;   OTHER INFORMATION: endothelial cell binding lipopeptide
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: 2 n hexadecylstearyl lysine
;   NAME/KEY: MOD_RES
;   LOCATION: (18)
;   OTHER INFORMATION: AMIDATION
US-09-925-715-12

  Query Match             56.1%;  Score 37;  DB 10;  Length 18;
  Best Local Similarity   81.8%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 AlKAlLkAlKA 14
              ||| | |||| |
Db          3 ALKLALKALKA 13


Search completed: August 21, 2003, 08:23:45
Job time : 55 secs
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